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Gaps
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Pred. No. 46;
1; Mismatches 0; Indels
    Length 20;
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09307200
Patent No. 6297215
GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Hancock, Nodra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,226C
PILING DATE: 10-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,857
FILING DATE: 31-MAY-1996
ATTORNEY-AGENT INPORMATION:
NAME: HAILS, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 36,347
REGISTRATION NUMBER: 36,347
REGISTRATION INPORMATION:
TELEPHONE: 619/678-5070
core 26; DB 3;
red. No. 46;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                        RESULT 14
US-08-763-226C-16
; Sequence 16, Application US/08763226C
; Patent No. 6057291
    89.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
Query Match
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-763-226C-16
                                                                                                              12 SSGPAL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 SSGPAL 17
                                                                                     1 SSGPSL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSGPSL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-307-200-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-658-8578-16
i Sequence 16, Application US/08658857B
patent No. 604435
i GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                   NAME/KEY: unsure
LOCATION: (656)
OTHER INFORMATION: Unidentified at time of filing
                                                                                                                                                                                                      LOCATION: (660)
OTHER INFORMATION: Unidentified at time of filling
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure

// LOCATION: (662)

OTHER HOPEN Unidentified at time of filing

US-09-351-215-4
                                                          OTHER INFORMATION: Unidentified at time of filing
                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: unsure
LOCATION: (661)
CTHER INFORMATION: Unidentified at time of filing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: MACOMPAILLE
COMPUTER: MACOMPAILLE
COMPUTER: MACOMPAIL
APPLICATION NUMBER: US/08/658,8578
FILING DATE: MAY 31, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,464
FILING DATE: June 2, 1955
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 3; 3
Pred. No. 1.3e+03;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/014001
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acide
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US-08-658-8578-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 SSGPSI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSGPSL 6
                                                                                                                                                                                      NAME/KEY: unsure
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us-09-848-834a-6.open.rai

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Best Local Similarity 83.3%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 0; Indels
STATE: CA
CCUNTRY: USA
ZIP: 92037
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTENG FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,200
FILING DATE:
APPLICATION NUMBER: US/09/307,200
FILING DATE:
APPLICATION NUMBER: 08/763,226
FILING DATE:
APPLICATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
FELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
TELEPHONE: APPLICATION NO: 16:
ENGTH: 20 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: APPLICATION
NOLECULE TYPE: peptide
US-09-307-200-16
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Search completed: March 10, 2004, 09:28:53 Job time : 3.32296 secs

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Sequence 13, Appl
Sequence 10, Appl
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Sequence 18, Appl
                                                                                                                                                  March 10, 2004, 09:16:59; Search time 26.7237 Seconds (without alignments) 268.645 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, A
Sequence 12, A
Sequence 11, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

l: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp;*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep;*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep;*
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16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep;*
17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep;*
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18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep;*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep;*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRPX 34
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US-10-297-942-12
US-10-295-074-11
US-10-295-074-13
US-10-297-942-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                      US-09-848-834A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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	equence 5,	equence 5,	equence 8,	29	14,	ď	ω̈	20	47	equence 9,	equence 15	18	equence 18.	equence 18	equence 180	equence 18	equence 2,	ö	equence 18	equence 49	equence 51	59	equence 53,	equence 17	equence 11	φ	equence 3,	equence 5,	Sequence 17, Appl		
	US-10-261-208-5	-10-295-074-	10-372-111-	-10-411-54	9-84	-10-297-94	10-297-94	-10-297-942-2	-10-295-07	-10-295-07	-10-29	-10-452-024-18	-10-452-024-18	-10-452-024-1	-10-452-024-18	-10-452-0	-09-816-467-	-10-452-024-1	-10-452-024-18	5-074-	-10-295-074-5	-10-295-074-	-10-295-074-5	-10-452-024-1	-10-130-973A-	-10 - 130 - 973	-10-130-973A-	-10-130-973A-	-130-973A-1	-10-130-973A-	
	14	14	15	15		14	44	14	14	14	14	15	15	15	15	15	10	15	15	14	14	14	14	15	14	14	14	14	14	14	
	21	21	21	32	37	158	158	158	194	285	287	441	441	444	451	452	463	469	472	514	514	514	517	573	605	665	882	907	1052	_	
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	16	17	78	13	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45	

ALIGNMENTS

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FEATURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 947-967 of t
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 947-967 of t
OTHER INFORMATION: Tetanus toxoid precursor (Tentoxylysin) linked by a spacer to a
OTHER INFORMATION: acid sequence 2-10 of the GnRH hormone
NAMB/KEY: MOD RES
LOCATION: (1) - (1)
OTHER INFORMATION: Amidated phenylalanine
NAMB/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(21)
OTHER INFORMATION: Amino acids 947-967 of the Tetanus Toxoid Precursor OTHER INFORMATION: (Tentoxylysin)
NAME/KEY: PEPTIDE
LOCATION: (22)...(25)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (26)...(34)
OTHER INFORMATION: Amino acids 2-10 of the human GnRH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
LOCATION: (34)...(34)
OTHER INFORMATION: Amidated glycine or glycinamide
                                                                                                                      TITLE OF INVENTION: Chimeric Peptide Immunogens TITLE OF INVENTION: Chimeric Peptide Immunogens FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR PAPLICATION NUMBER: 60/202,328
PRIOR PAPLICATION NUMBER: 60/202,328
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 10
LENGTH: 34
US-09-848-834A-10

; Sequence 10, Application US/09848834A

; Patent No. US20020076416A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Appli Appli Appl

Sequence 3, 1 Sequence 4, 1 Sequence 6, 1 Sequence 2, 5 Sequence 6, 1

US-09-943-548-3 US-09-848-834A-4 US-09-785-215-6

Sequence Sequence B

US-10-204-362-6 US-10-204-362-6 US-10-339-522-3 US-10-223-711-8 US-10-223-809A-6

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FEATURE:
OTHER INFORMATION: hTWF with inserted tetanus toxoid P2 and P30 epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS FILE REFERENCE: P1013DK00 CURRENT APPLICATION NUMBER: US/10/295,074 CURRENT FILING DATE: 2002-11-15 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin version 3.1 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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64.0%; Score 119; DB 14; Length 194;
Best Local Similarity 81.5%; Pred. No. 3.6e-08;
Matches 22; Conservative 1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                 ?
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
NUTAGEN
LOCATION: (125). (145)
OTHER INFORMATION: Tetanus toxoid P30 epitope (SEQ ID NO: SEATURE:
NAME/KEY: MSC_PEATURE
LOCATION: (2). (109)
OTHER INFORMATION: hTNF amino acids 1-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (110)..(124)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCS-10-297-942-12

Sequence 12, Application US/10297942

Sequence 12, Application US/10297942

PUBLICANT: FOR MCS-1020030185816A1

APPLICANT: Ferring BV

TITLE OF INVENTION: Solubilised Protein Vaccines

FILE REFERENCE: F08445U50

CURRENT APPLICATION NUMBER: US/10/297,942

PRICR APPLICATION NUMBER: PCT/DK01/00431

PRICR FILING DATE: 2001-10-16

PRICR FILING DATE: 2001-10-16

PRICR FILING DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN NOS: 20

SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
63.4%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (146)..(194)
OTHER INFORMATION: hTNF amino acids 109-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 FNNFTVSFWLRVPKVSASHLEAEAKFW 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FUNFTVSFWLRVPKVSASHLEGPSLHW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 FUNFTVSFWLRVPKVSASHLEG 154
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-297-942-12
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-295-074-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human OTHER INFORMATION: Gard linked by a spacer to amino acid sequence 947-967 of the Tet OTHER INFORMATION: amis toxoid precursor (Tentoxylysin) profesin linked by a spacer to OTHER INFORMATION: o amino acid sequence 2-10 of human Gard NAME/KEY: MOD_RES INCORATION: o amino acid sequence 2-10 of human Gard NAME/KEY: MOD_RES INCORATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD_RES INCORATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD_RES INCORATION: Amidated glycine or glycinamide
NAME/KEY: PEPTIDE
LOCATION: (1)...(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (17)..(37)
OTHER INFORMATION: Amino acid sequence 947-967 of the Tetanus toxoid precursor (Tend
OTHER INFORMATION: oxylysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KEY: PEPFILES
LOCATION: (11)..(16)
OTHER INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE

LOCATION: (42)..(50)

COTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone US-09-848-8348-18
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                                                              Query Match
99.5%; Score 185; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 33; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-848-834A-18
Sequence 18, Application US/09848834A
Facent No. US20020076416A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE REFERENCE: 1102865-0047
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 06/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.5%; Score 185; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                          1 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (38)..(41)
OTHER INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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                 US-09-848-834A-10
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LENGTH: 50
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RESULT 5 US-10-295-074-11 ; Sequence 11, Application US/10295074

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GENERAL INFORMATION:
APPLICANT: Ritershaus, Charles W.
APPLICANT: Ritershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVIT TITLE OF INVENTION: MODULATION OF S. 11.1P US-2
CURRENT APPLICATION NUMBER: US/0943.548
CURRENT FILING DATE: 2001-08-30
CURRENT FILING DATE: 1995-05-01
PRIOR PRILING DATE: 1996-05-01
PRIOR PRILING DATE: 1996-05-01
PRIOR FILING DATE: 1996-05-01
PRIOR FILING DATE: 1997-10-17
SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LIBRIDAL
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                                                                                                                   61.3%; Score 114; DB 14; Length 158; 70.6%; Pred. No. 1.4e-07; ive 0; Mismatches 2; Indels
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60.2%; Score 112; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 21; Conservative 0; Mismatches 0; Indels
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LOCATION: (1)..(21)
OTHER INFORMATION: Amino acid sequence 947-967 of Tetanus
OTHER INFORMATION: Toxoid Precursor (Tentoxylysin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: helper T cell epitope of tetanus toxin US-09-943-548-3
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Patent No. US20020076416A1

GENERAL INFORMATION

APPLICANT: Aphton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

TITLE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION UNMER: 60/202,328

PRIOR APPLICATION UNMER: 60/202,328

NUMBER OF SEQ ID NOS: 20

SEQ ID NOS: 20

SEQ ID NO 4

ILENGTH: 21
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                                                                                                                                                                                                                                                                       41 FNNFTVSFWLRVPKVSASHLBQVLFKGQGCPSTH 74
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; Sequence 3, Application US/09943548
; Patent No. US20020042364A1
; GENERAL INFORMATION:
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                                                                                                                                                                            Conservative
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-942-10
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-848-834A-4
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US-10-295-074-13
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; OTHER INFORMATION: 2 human IL5 monomers joined by P2 and P30 epitopes US-10-295-074-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                        APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REPREBNCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 285
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Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL INMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT ELIMO ADDRE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 14;
Pred. No. 1.4e-07;
1; Mismatches 1;
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62.4%; Score 116; DB 14;
Best Local Similarity 91.7%; Pred. No. 1.4e-07;
Matches 22; Conservative 1; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 22; Conservative
        Publication No. US20030185845A1
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LENGTH: 287
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Sequence 6, Application US/10204362
Publication No. US20030086938A1
GENERAL INFORMATION:
APPLICANT: MEE Biotech A/S
TITLE OF INVENTION: No. US20030086938A1e1 Method For Down-Regulation Of Amyloid
TITLE OF INVENTION: No. US20030086938A1e1 Method For Down-Regulation Of Amyloid
TITLE OF INVENTION: NO. US20030086938A1e1 Method For Down-Regulation Of Amyloid
CURRENT APPLICATION NUMBER: US/10/204,362
CURRENT FILING DATE: 2002-08-16
SOFTWHARE: Patentin Ver. 3.0
SEQ ID NO 6.
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APPLICANT: Kaumaya, Pravin T.P.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
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; Publication No. US20030113344A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     ; TYPE: PRT;
; ORGANISM: Clostridium tetani
US-10-204-362-6
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Matches 21, Conservative
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APPLICANT: CANTACUZENE, Daniele
APPLICANT: CANTACUZENE, Daniele
APPLICANT: LECLERC, Claude
APPLICANT: LO-MAN, Richard
TITLE OF INVENTION: WULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE, VACCINE
TITLE OF INVENTION: COMPRISING THE SAME AND USE THEREOF
TITLE OF INVENTION: COMPRISING THE SAME AND USE THEREOF
FILE REFERENCE: 1341 US 3565
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 60/041,726
EARLIER FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
LENGTH: 21
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Publication No. US20020187157A1
Publication No. US20020187157A1
APPLICANT: JENSEN, Martin Roland et al.
TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID CURRENT APPLICATION NUMBER: US/09/785,215
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 6.
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Pred. No. 3e-08;
                                                              Query Match

60.2%; Score 112; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 21; Conservative 0; Mismatches 0; Indels
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60.2%; Score 112; DB
Best Local Similarity 100.0%; Pred. No. 3e-
Matches 21; Conservative 0; Mismatches
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; ORGANISM: Clostridium tetani
US-09-405-986-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-785-215-6
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US-10-204-362-6
                       US-09-848-834A-4
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US-09-785-215-6
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JUNIORATION NO. US2003015711741
Sequence 6, Application US/10223809A
Publication No. US2003015711741
GENERAL INFORMATION:
JAPPLICANT: Rasmussen, Peter Birk et al.
APPLICANT: Rasmussen, No. US20030157117A1el Method for Down-Regulation of Amyloid
TITLE REFERENCE: 674542-2008
CURRENT APPLICATION NUMBER: US/10/223,809A
CURRENT APPLICATION NUMBER: US 60/337,543
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-10
PRIOR PRIOR APPLICATION NUMBER: DE 2001 01231
PRIOR APPLICATION NUMBER: DE 2001 01231
PRIOR APPLICATION NUMBER: DE 2001 06-8
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: DE 2002 0058
PRIOR APPLICATION NUMBER: DE 2002 0058
PRIOR PILING DATE: 2002-04-16
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
TYPE: PRT
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TYPE: PRT
CRANISM: Clostridium tetani
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FILE REFERENCE: 18525/04058
CURRENT APPLICATION NUMBER: US/10/223,711
CURRENT FILING DATE: 2002-08-19
FRIOR APPLICATION NUMBER: 09/148,711
PRIOR PILING DATE: 1908-09-04
PRIOR PILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Version 3.1
SENGTH: 21
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; ORGANISM: Clostridium tetani
US-10-223-711-8
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US-10-223-809A-6
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Search completed: March 10, 2004, 10:25:48 Job time : 26.7237 secs

28kzm3 clostridium

Q9far6 clostridium Q8far6 clostridium Q8h35 clostridium Q9h35 clostridium Q9h25 clostridium Q9h26 clostridium Q9h26 clostridium Q9h26 clostridium Q9h26 clostridium Q9h26 clostridium Q9h27 comato spot Q8 x39 comato spot Q8 x30 comato spot Q8 x20 comato spot Q8

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
12-Clostridium tetani.
12-Clostridium tetani.
13-Clostridium.
14-Clostridium.
15-Clostridium.
16-Clostridium.
17-Clostridium.
18-Clostridium.
18-Clostridium.
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He H.J., Shi H.J., He Z.Y., Yuan Q.S., Wu X.F.;
He H.J., Shi H.J., He Z.Y., Yuan Q.S., Wu X.F.;
I "Fragment C of Tetanus Toxin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AFI54828; AAF73267.1;
HSSP; P04958; 1A8D.
GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
R InterPro; IPR00895; ConA like lec_gl.
InterPro; IPR00895; ConA like lec_gl.
InterPro; IPR001064; Crystallin.
R InterPro; IPR002160; Kunitz legume.
R PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
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100.0%; Pred. No. ...
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Q8L853
Q6L853
Q9EM45
Q9EM61
Q9DER1
Q9DER1
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Q8CZYC
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Q8WVD0
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Q93PY5
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Query Match
Best Local
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Q45861 clostridium
Q45862 clostridium
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRPX 34
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_nman:*
5: sp_nvertebrate:*
5: sp_vvertebrate:*
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

Q7YKK8

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Gaps

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Indels

Score 112; DB 2; Length 451; Pred. No. 1.5e-07;

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[3]
SEQUENCE OF 635-1000 FROM N.A.
SEQUENCE OF 635-1000 FROM N.A.
MEDLINE-94013372; PubMed-8408542;
Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.",
J. Clin. Microbiol. 31:2255-2262(1993).
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MEDLINE=S9640102; PubMed=9732534;
MEDLINE=S9640102; PubMed=9732534;
MEDLINE=S9640102; PubMed=17826

"Analysis of the botulinum neurotoxin type F gene clusters in proteolytic and nonproteolytic Clostridium botulinum and Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI TaxID=1491;
GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0009405; P:pathogenesis: IEA.

GO; GO:000508 P:proteolysis and peptidolysis; IEA.

R InterPro; IPR002160; Kunitz_legume.

InterPro; IPR002160; Kunitz_legume.

InterPro; IPR002160; Kunitz_legume.

InterPro; IPR002150; Peptidase M27.

InterPro; IPR00125; Peptidase M27.

R PAGM; PP01742; Peptidase W27; I.

R RINTS; PR00760; BONTOXILYSIN.

PROSITE; PS001963; BONTOXILYSIN.

R PROSITE; PS001963; BONTOXILYSIN;

R PROSITE; PS001963; BONTOXILYSIN;

R SEQUENCE 1268 AA; 145513 MW; 963040091ACI5ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1268;
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0008270; F:toxin activity; IEA.
GO; GO:0009405; P:tainc ion binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
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STRAIN=NCTC 10281;
Hutson R.A. Collins M.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binore M.J., Bodsworth N.J., Whelan S.M., Minton N.P., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057236, Q45863,
01-NOV-1996 (TEMBLEEL 01, Created)
01-NOV-1996 (TEMBLEEL 01, Last sequence update)
01-NOT-2003 (TEMBLEEL 25, Last annotation update)
Botulinum neurotoxin type F (BONT/F protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
33.3%; Score 62; DB 2;
Best Local Similarity 64.3%; Pred. No. 6.5;
Matches 9; Conservative 4; Mismatches
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EMBL; X81714; CAA57388.1; --
EMBL; L35496; AAA2310.1; --
EMBL; X70821; CAA50152.1; --
EMBL; X99064; CAA67512.1; --
PIR; 548110; S48110.
HSSP; P10445; 3BTA.
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MEDLINE=9328228; PubMed=8486245;

A MEDLINE=9328228; PubMed=8486245;

Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,

Richardson P.T.;

"Nucleotide Sequence of the gene coding for Clostridium barati type F.

"Nucleotide Sequence of the gene coding for Clostridium barati type F.

"Nucleotide Sequence of the gene coding for Clostridium barati type F.

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                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tetanus toxin (Fragment).
Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Clostridium baratii.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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Pred. No. 5e-07;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                   Further State of the state of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1310 1310
1310 AA; 150316 MW; 9EADDC914418E450 CRC64;
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           PRT; 1310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  948 FNNFTVSFWLRVPKVSASHLE 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 60.2%; Scc
Local Similarity 100.0%; Pr
es 21; Conservative 0;
           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1561;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1513;
                                                                                                                                                                                                                                                                                              Clostridium.
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                                    STRAIN=type B;
MEDLINE=94013372; PubMed=8408542;
Gampbell K., East A.K., Collins M.D.;
"Gemp probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
BENBL; X70814; CAA50145.1; -.
HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional characterisation of tetanus and botulinum neurotoxins binding domains.";
J. Cell Sci. 112:2715-2724(1999).

EMBL; AJ242628; CAB43706.1; -.
HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
NCBI_TaxID=1491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=9934361; PubMed=10413679;
Lalli G., Herreros J., Osborne S.L., Montecucco C., Rossetto O.,
Schiavo G.;
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                                                                                                                                                                                                                                                                                                       Score 58; DB 2; Length 361;
Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004866; F:endopeptidase inhibitor activity; IEA. GO; GO:0015070; F:toxin activity; IEA. InterPro; IRR008985; ConA like lec_gl. InterPro; IPR002160; Kunitz_legume.
                                                                                                                                                                                                                                                     361 361 361 361 533EA98735CD98E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 AA; 52772 MW; 721D0B468E8C95A4 CRC64;
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Botulinum neurotoxin type B (Fragment).
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                              GO; GO: 0015070; F: toxin activity; IEA.
Interpro; IPR008985; ConA_like_lec_gl.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 64.3%;
Marches 9; Conservative
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Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     290 FLDFSVSFWIRIPK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FUNFTUSFWLRUPK 14
                                                                                                                                                                                                                                                                                                                                                                                  1 FUNFTVSFWLRVPK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 FLDFSVSFWIRIPK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                     SEQUENCE FROM N.A.
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Q9ZAJ8
ID Q9ZA
AC Q9ZA
DT 01-M
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MEDLINE=94013372; PubMed=8408542;
Campbell K., East A.K., Collins M.D.;
Campbell K., East A.K., Collins M.D.;
Gene probes for identification of the botulinal neurotoxin gene and
specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262 [1993].
HSSP; P10845; 3BTA.
GO; GO:0015070; F:toxin activity; IEA.
InterPro; IPR008985; ConA_like_lec_gl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                               / Match 32.8%; Score 61; DB 2; Length 1278; Local Similarity 57.1%; Pred. No. 9.2; see 8; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.2%; Score 58; DB 2; Length 361; 64.3%; Pred. No. 6; 1: Indels :ive 4; Mismatches 1; Indels
                                                                                                                                                                                1278 AA; 147073 MW; AIBE1318431D6918 CRC64;
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361 361 361
361 AA, 42131 MW, AZEOFFFC81F9533D CRC64;
Q45848 PRELIMINARY, FK1; SOL AND Q45848; O1-NOV-1996 (TYENBLEE]. 01, Created) 01-NOV-1996 (TYENBLEE]. 01, Last sequence update) 01-OCT-2003 (TYENBLEE]. 25, Last amnotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botulinum neurotoxin type B (Fragment)
BONT/B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulinum neurotoxin type B (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|:||||:||
290 FLDFSVSFWIRIPK 303
                                                                                                                                                                                                                                                                                                               931 YONFSISFWVRIPK 944
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                                                                                                                                                                                                                                                                                          1 FUNFTVSFWLRVPK 14
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
NCBI_TaxID=1491;
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Q45846;
                                                                                                                                                                                                                                                         Matches
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Q45848
ID Q458
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Q45846
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XITAMA N. 'Perreira and 588;

XITAMA N. 'Perreira and J., Baumstark B.R.;

Contain type B toxin gene sequences.";

SUBMINITION OF SALING STAND GENERAL/DOBJ databases.

SUBMINITION OF ALMINING STAND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type B cryptic neuroccain.
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia, Clostridiales, Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                         Length 1291;
        Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXII/SIN.
ProDom; PD001963; BONTOXII/Sin; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
SEQUENCE 1291 AA; 150824 MM; D7CA07BAE2EBBCD2 CRC64;
                                                                                                                                                                                                                                                                                                                     Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                     Query Match 31.2%; Score 58; DB 2; Best Local Similarity 64.3%; Pred. No. 25; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1291 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         923 FLDFSVSFWIRIPK 936
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Best Local Similarity 64.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-NOV-1996 (
01-NOV-1996 (
01-OCT-2003 (
BONT/B.
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Q08077
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"Characterization of six type A strains of Clostridium botulinum that

"Characterization of six type A strains of Clostridium botulinum that

"Characterization of six type A strains of Clostridium botulinum that

submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF295926, AMS7132.1;

GO, GO:0008237; F:metallopeptidase activity; IEA.

GO, GO:0008237; F:metallopeptidase activity; IEA.

GO, GO:0008270; F:ranc ion binding; IEA.

GO, GO:0008405; P:pathogenesis; IEA.

GO, GO:0008405; Cond. like lec.

InterPro; IPR002160; Kunifz_legume.
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                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE=98440323; PubMed=9767710; Santos-Buelga J., Collins M.D., East A.K.; Collins M.D., East A.K.; Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & F
                                                                                Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
COSTRIGIUM.
COSTRIGIAND=1491;
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Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A GO; GO: 000826; SHEAD AGO GO: 000866; F: endopeptidase inhibitor activity; IEA. GO; GO: 000827; F: endopeptidase activity; IEA. GO; GO: 0008270; F: endopeptidase activity; IEA. GO; GO: 0008270; F: ainc activity; IEA. GO; GO: 0008405; F: ainc activity; IEA. GO; GO: 0008405; F: ainc an binding; IEA. GO; GO: 0009405; P: pathogenesis; IEA. GO; GO: 0009405; P: pathogenesis; IEA. RILTEPPRO; IPR002186; CANAILE LEG_GI.

R InterPro; IPR002186; CANAILE LEG_GI.
R InterPro; IPR002186; Peptidase M27. InterPro; IPR000395; Peptidase M27. InterPro; IPR001865; Peptidase M27. R Pfam; PF01742; Peptidase M27; I. R PRNNTS; PR00742; Peptidase M27; I. R PRNNTS; PR001863; BONTOXIIYSIN.
R ProDom; PD01963; BONTOXIIYSIN.
R PROSITE; PS001843; ZINC PROTEASE; I. SEQUENCE 1291 AA; 150840 MW; E4D3B0E46AB2E735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.2%; Score 58; DB 2; Length 1291; 64.3%; Pred. No. 25; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BonT protein.
BonT.
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3630; CAA73968.1; -.
0845; 3BTA.
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InterPro, IPR000395; Peptidase_M27
InterPro, IPR006025; Pept_M_Zn_BS.
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923 FLDFSVSFWIRIPK 936
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Les 9; Conservative
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CDC 3281;
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STRAIN=1436;
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Best Loc Matches

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RESULT 9 093G71

DER RETARDED DE LA PACE DE LA PAC

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Gaps

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MEDLINE=21128526; PubMed=11207749;
Smits T.H.M., Roethlisberger M., Witholt B., Van Beilen J.B.;
Smoteriar screening for alkane hydroxylase genes in Gram-negative and
Gram-positive bacteria.";
Environ. Microbiol. 1:307-317(1999).
                                                                                                                                                             Gaps
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STRALN-A31(2), M145,
MEDILINE-1996410; Pubbed-12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.

NCBI_TaxID=1902;
                                                                                                         Length 1291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 57; DB 2; Length 430; 35.9%; Pred. No. 10; 7; Indels iive 4; Mismatches 7; Indels
Prodom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
SEQUENCE 1291 AA; 150574 MW; 0227CAEF4F58504D CRC64;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ009579; CAB51045.2; -.
GO; GO:0018683; F:camphor 5-monooxygenase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR005804; FA desar fam.
Pfam, PR00487; FA desarturaes; 1.
Monooxygenase; Oxidoreductase.
SEQUENCE 430 AA; 48337 MW; 048E950980783E86 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Putative transmembrane protein.
SCO3902 OR SH24.144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Alkane 1-monooxygenase (EC 1.14.15.1).
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                                                                                                         Score 58; DB 2
Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             430 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                         31.2%;
ilarity 64.3%;
Conservative
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923 FLDFSVSFWIRIPK 936
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les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas fluorescens.
                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=294;
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Matches
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Q9XAV1
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Thara H., Kohda T., Morimoto F., Tsukamoto K., Karasawa T.,
Nakamura S., Mukamoto M., Kozaki S.;
"Clostridium botulinum type B neurotoxin associated with infant
                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=EXLUNG 17B ATCC25765,
MEDLINE=9412559; Pubbed=7764370;
Hutson R.A., Collins M.D., East A.K., Thompson D.E.;
"Nucleocities sequence of the gene coding for non-proteolytic
"Nucleocities sequence of the gene coding for non-proteolytic
Clostridium botulinum type B neurotoxin: comparison with other
clostridial neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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(G) GO:0004866; F:endopeptidase inhibitor activity; IEA.

(G) GO:000537; F:metallopeptidase activity; IEA.

(G) GO:000507; F:metallopeptidase activity; IEA.

(G) GO:000507; F:toxin activity; IEA.

(G) GO:0009405; F:pathogenesis; IEA.

(G) GO:0009405; P:pathogenesis; II.

(G) GO:0009406; P:pathogenesis; II.

(G) GO:
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Pred. No. 25;
4; Mismatches 1; Indels
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botulism.";

submitteed (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB08415.; BAC22064.1; -

GO; GO:000827; F:netallopeptidase inhibitor activity; IEA.

GO; GO:000827; F:netallopeptidase activity; IEA.

GO; GO:0008207; F:netallopeptidase activity; IEA.

GO; GO:0008405; F:toxin activity; IEA.

GO; GO:0009405; F:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR002160; Kunitz legume.

InterPro; IPR002160; Kunitz legume.

InterPro; IPR000395; Peptidase_M27.

INTERPROSECTION INTERPROSECTIO
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Last annotation update)
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EMEL, X7143; CAA50482.1; -.
PIR; 140631; 140631.
HSSP; P10845; 3BTA.
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| 923 FLDFSVSFWIRIPK 936
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les 9; Conservative
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NCBI_TaxID=1491;
                                        NCBI_TaxID=1491;
        Clostridium
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297 YKNFSISFWVRIPNYDNKIVNVNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQ 356
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"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
EMBU, X70818; CAA50149:1;
PIR; S48106; S48106.
Thomson N.R., James K.D., Harris D.E., Quail. M.A., Kieser H., Bareman A., Brown. S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Eabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Harren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill JJ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BONT/E.
Clostridium botulinum.
Clostridium botulinum.
Clostridium.
Clostridium.
NCBI_TaxID=1491;
                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
Nature 417:141-147(2002).
PIR, T36589; T36589.
PIR, T36589; T36589.
Transmembrane; Complete proteome.
SEQUENCE 502 A4; 54795 MW; C84F774C0A5AADBC CRC64;
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30.4%; Score 56.5; DB 2; Length 367;
Best Local Similarity 22.4%; Pred. No. 9.9;
Matches 15; Conservative 8; Mismatches 7; Indels 3:
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367 367
367 AA; 42902 MW; 346A610C2FF70262 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 AA
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GO; GO:0015070; F:toxin activity; IEA.
InterPro; IPR008985; ConA_like_lec_gl.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MEDLINE=94013372; PubMed=8408542;
                                                                                                                                                                                                                                                                                                                                                                          18 SHLEGPSLHWSYGLRP 33
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357 KLAFNYG 363
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                                                                                                                    Hopwood D.A.;
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SEQUENCE
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Q45861
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Search completed: March 10, 2004, 09:25:33 Job time : 35.6031 secs

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Immunogen
T-celaus t
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Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
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luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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/note= "Tetanus toxoid sequence (947-967 aa)"
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AAW67034
AAW67579
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AAY92626
AAY99876
                                  AAY84426
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Copyright (c) 1993 - 2004 Compugen Ltd.
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14-APR-1994;
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10-SEP-1995
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                                   The invention relates to a synthetic immunogen for inducing specific antibodies against gonadorropin releasing hormone (GnRH also known as luteinishing hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, therus and other gynaccological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
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/note= "Gonadotrophin releasing hormone epitope (1.
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'note= "Other= Pyro-glutamic acid or 5-oxo
                                                                                                                                                                                                Length 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11. .16
/note= "Spacer peptide"
17. .37
/note= "Tetanus toxoid (947-967 aa)"
                                                                                                                                                                                              99.5%; Score 185; DB 5; L
100.0%; Pred. No. 8.2e-20;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                       8. .41
note= "Spacer peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ocation/Qualifiers
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                    Claim 11; Page 7; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                           Synthetic immunogen peptide 10.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                        Local Similarity 100. es 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                           Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
  or its analog.
                                                                                                                                                                                                                                                                                                                                                       12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                   AAU11429;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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Matches
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Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper I-cell peptide epitope and immunomimic peptide epitope or its analog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH also known as luteinising hormone releasing hormone, HRRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 99.5%; Score 185; DB 5; L
Local Similarity 100.0%; Pred. No. 1.3e-19;
nes 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 FINFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FUNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHRH-containing immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23. .32
/note= "LHRH hapten"
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                                                                                                                             Stevens VC;
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94US-00229275.
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05-MAY-2000; 2000US-0202328P
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(first entry)
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/note=
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                                                                                                                             Grimes S, Michaeli
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                                                                  (APHT-) APHTON CORP
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98DK-00001261 98US-0105011P

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(MEBI-) M & E BIOTECH AS
           05-OCT-1998;
20-OCT-1998;
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                                                                                                                                               synthetic immunogenic peptides are protect in which a universal immune stimulator is linked to a peptide or protein hapten containing soll and/or cytotoxic T lymphocyte epitopes, giving a product which causes of potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiseuous halper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HiA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of yersinia Spacer amino acid commains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator and hapten components an LHRH. Containing, invasin-free immunogenic peptide as above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgence dependent carcinoma, prostatic carcinoma, testicular carcinoma, androgence endometriosis, benign uterine tumours, recurrent functional ovarian
                                                                                                                                         Synthetic immunogenic peptides are provided in which a universal immune
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate specific membrane antigen; immunogenized construct; mutant; vaccination; cytotoxic T-lymphocyte immunity; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope.
                                                                                                                                                                                                                                                                                                                                cancer, (severe) premenstrual syndrome or oestrogen-dependent breast cancer, or for induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant human prostate specific membrane antigen construct, hPSM1.10
                                                                               Immunogenic luteinising hormone releasing hormone peptide(\theta) - that suppress LHRH activity in males and females.
                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     81.7%; Score 152; DB 2;
87.9%; Pred. No. 5.6e-15;
live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              573. .693
/label= p30
/note= "foreign epitope"
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24. .38
/label= P2
/note= "foreign epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY92633 standard; protein; 750 AA
                                                                                                                 Claim 8; Page 84; 213pp; English
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                                   Zamb T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 87.9'
                                                          WPI; 1994-357910/44.
                                   Ladd AE, Wang CY,
WANG C Y.
ZAMB T.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32 AA;
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Synthetic.
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Peptide
           (ZAMB/)
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AAY92627-49 are mutant immunogenized human prostate specific membrane antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30). The immunogenic analogues of PSM can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. The method is used for inducing immune responses against weakly immunogenize cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human proteits especific membrane antigen (PSM), hereapolla? (Her2) and/or fibroblast growth factor 8b (PGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL cytocoxic T-lymphocyte) croup derived from the PA and/or at least 18-cell group derived from the cell-associated PA, and (2) at least 1 E-cell group derived from the cell-associated PA, and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of the respective PA and including at least one foreign T helper epitopes are also claimed. The method is used to treat prostate, prostate, breast or respective PA and including to the treat prostate, prostate, breast or breast cancer when the PA is human PSM, FGP8b and Har2, respectively. Which appears on pages 184-187 of the bard of the wild type human PSM (AAY92619), which appears on pages 184-187
                                                                                                                                                                Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer.
Dalum I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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Leach D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Haaning J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 121.5; DB 3;
Pred. No. 6.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated human CEA-TT P2 and P30 epitopes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            673 FNNFTVSFWLRVPKVSASHLE-PSSHNKY 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FNNFTVSFWLRVPKVSASHLEGPSLHWSY 29
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/note= "signal peptide"
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Nielsen KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                   Example 1; Page; 220pp; English.
                                Birk P, Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
   Mouritsen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35. .537
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                                                                                                WPI; 2000-349917/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 750 AA;
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   Steinaa L,
                                       Sautam A,
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ABR82481
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WPI; 2003-587260/55
        (PHAR-) PHARMEXA AS
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                             Klysner S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                             The invention relates to inducing an immune response against autologous carcinoembryonic antigen (CEA) in an animal, e.g. human. The method involves effecting uptake and processing by antigen presenting cells (APCS) in the animal of at least 1 modified CEA polypeptide or of a mucleic acid encoding the modified CEA polypeptide or of a microorganism or virus expressing the modified CEA polypeptide to induce a CTL response and an antibody response that targets the autologous CEA. The method is useful in immunizing actively against diseases characterized by cells that express CEA. The present sequence represents a truncated human CEA polypeptide that has tetanus toxoid (TT) P2 and P30 epitopes introduced
                                                                                                                                       Inducing an immune response in humans against autologous carcinoembryonic antigen (CEA) comprises administering a modified CEA polypeptide, a nucleic acid encoding the polypeptide, or a microorganism expressing the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CBA; immune response; carcinoembryonic antigen; antigen presenting cell; APC; cytostatic; vaccine; human; tetanus toxoid; p2; p30; antigen.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                          65.1%; Score 121; DB 7; Length 537; 95.8%; Pred, No. 5.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified human CEA-TT P2 and P30 epitopes
                                                                                                                                                                                             Disclosure; Page 134-137; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                   1 FNNFTVSFWLRVPKVSASHLEGPS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR82479 standard; protein; 708 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2003; 2003WO-DK000031
                    17-JAN-2003; 2003WO-DK000031.
                                        17-JAN-2002; 2002DK-00000082.
17-JAN-2002; 2002US-0350047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 95.8
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .34
/note=
                                                                                         Voldborg B;
                                                                                                              WPI; 2003-587260/55.
N-PSDB; ACF35968.
                                                                        (PHAR-) PHARMEXA AS
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                                                                                                                                                                                                                                                                                                                                          Sequence 537 AA;
                                                                                                                                                                                                                                                                                                                       in its sequence
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                                                                                           Klysner S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                   Inducing an immune response in humans against autologous carcinoembryonic antigen (CEA) comprises administering a modified CEA polypeptide, a nucleic acid encoding the polypeptide, or a microorganism expressing the polypeptide.
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0
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Best Local Similarity 88.5%; Pred. No. 7.3e-09;
Matches 23; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified human CEA-TT P2 and P30 epitopes.
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 121-124; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .34
/note= "signal peptide"
35. .717
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 FNNFTVSFWLRVPKVSASHLEIPQQH 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR82478 standard; protein; 717 AA.
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17-JAN-2002; 2002US-0350047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2003; 2003WO-DK000031
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Voldborg B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klysner S, Voldborg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAR-) PHARMEXA AS
                                                                        WPI; 2003-587260/55.
                                                                                                          N-PSDB; ACF35966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 708 AA;
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Mouritsen S;

Voldborg B,

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The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (115) and tumnour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is human TNFalpha variant protein with an inserted tetanus toxoid P2 and P30 epitopes. This sequence is used to illustrate the method of the invention
                                                                                                                                                       New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%; Score 119; DB 6; Length 194;
81.5%; Pred. No. 3.2e-09;
Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 FUNFTVSFWLRVPKVSASHLEAEAKPW 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FNNFTVSFWLRVPKVSASHLEGPSLHW 27
                                                                                                                                                                                                                              Claim 23; Page 158; 196pp; English.
                                                                    Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY92655 standard, peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                    Klysner S, Nielsen FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-349917/30.
                        (MOUR/) MOURITSEN S
                                                                                                           WPI; 2003-449558/42
  VOLDBORG B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 194 AA;
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20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY92655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
  (/dTOA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                   The invention relates to inducing an immune response against autologous carcinoembryonic antigen (CEA) in a animal, e.g. human. The method involves effecting uptake and processing by antigen presenting cells (APCs) in the animal of at least 1 modified CEA polypeptide or of a microcrossing or virus expressing the modified CEA polypeptide or of a microcrosganism or virus expressing the modified CEA polypeptide or of a microcrosganism or virus expressing the modified CEA polypeptide or of a microcrosganism or virus expressing the modified CEA polypeptide or of a microcrosganism or virus expressing the modified CEA polypeptide to induce a CTL response and an antibody response that targets the autologous CEA. The method is useful in immunizing actively against diseases characterized by calls that express CEA. The present sequence represents a modified human CEA polypeptide that has tetanus toxoid (TT) P2 and P30 epitopes introduced
                                         Inducing an immune response in humans against autologous carcinoembryonic antigen (CEA) comprises administering a modified CEA polypeptide, a nucleic acid encoding the polypeptide, or a microorganism expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multimeric protein; interleukin 5; IL5; TNPalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; human; mutant; mutein; variant; tetanus toxoid; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.1%; Score 121; DB 7; Length 717; 95.8%; Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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/hote= "Tetanus toxoid P2 epitope"
125. .145
/hote= "Tetanus toxoid P30 epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                              Disclosure; Page 114-117; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNNFTVSFWLRVPKVSASHLEGTS 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human INFalpha variant, INF34-P2-P30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO30488 standard; protein; 194 AA
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/note= "Human TNF"
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'note= "Human TNF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5-NOV-2002; 2002WO-DK000764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2001; 2001DK-00001702.
16-NOV-2001; 2001US-0331575P.
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KLYSNER S.
NIELSEN F S.
BRATT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
N-PSDB; ACF35964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 717 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           in its sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Unidentified.
Chimeric.
                                                                                                                polypeptide.
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(KLYS/)
(NIEL/)
(BRAT/)
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Region
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Gaps

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Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer.
                                                             Foreign epitope, P2, prostate specific membrane antigen, vaccination, cytotoxic T-lymphocyte immunity, self-protein, cancer, breast cancer, prostate cancer, cell-associated peptide antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leach D,
PSMpep012 - P30 inserted in hPSM insertion position 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steinaa L, Mouritsen S, Nielsen KG, Haaning J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 118; 220pp; English.
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birk P, Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DK-00001261.
98US-0105011P.
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/label= P30
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AAY92650-55 are peptides designed which correspond to the P2 and P30 epitopes with 5 flanking human prostate specific membrane antigen (hPSM) amino acids in each end. The flanking amino acids correspond to the epitope insertion sites 6, 8 and 10. The peptides will be used in, e.g. T cell proliferation assays, but also for ELISA or other in vitro assays.

The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, hPSM, herequlin 2 (Herz) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (i) at least 1 CTL (cytotoxic T-1) ymphocyte) group derived from the PA and/or at least 1 B-cell group cell group which is foreign to the animal. Analogues of human PSM, human are least one foreign to the animal. Analogues of human PSM, human are least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed. The method is used to treat prostate/breast or breast cancer when the PA is human PSM, FGF8b and Herz, respectively

Sequence 31 AA;

Gaps 1; Query Match 63.7%; Score 118.5; DB 3; Length 31; Best Local Similarity 92.3%; Pred. No. 4.6e-10; Matches 24; Conservative 0; Mismatches 1; Indele 1

1 FNNFTVSFWLRVPKVSASHLEGPSLH 26

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RESULT

AAW81336 standard; protein; 158 AA. AAW81336

AAW81336;

21-APR-1999 (first entry)

INF30-5, a TWF-alpha analogue.

Human tumour necrosis factor-alpha, TNF-alpha; TNF-alpha analogue, vaccine, rheumatoid arthritis, Crohn's disease, ulcerative colitis, cancer, disseminated sclerosis, diabetes; psoriasis, osteoporosis, asthma.

Synthetic

Homo sapiens.

WO9846642-A1

22-OCT-1998

98WO-DK000157. 15-APR-1998; 97DK-00000418. 97US-0044187P. 15-APR-1997; 24-APR-1997;

(FERR) FARM LAB FERRING AS

Dalum I; Elsner H, Jensen MR, Mouritsen S,

WPI; 1998-594561/50. N-PSDB; AAV68425. Modified human tumour necrosis factor-alpha - comprises immunodominant \mathtt{T} cell epitope, useful in vaccines to treat or prevent TNF-associated diseases, e.g. cancer.

Claim 15; Page 81-82; 134pp; English.

The present sequence represents a modified human tumour necrosis factor-

alpha (TNF-alpha) analogue. The analogues have no residual TNF activity and are immunogenic in a large proportion of the human population (by using promiscuous epitopes). The TNF-alpha analogue is able to generate, in humans, neutralizing antibodies to wild-type human TNF alpha, has at least one fragment of TNF substituted by a peptide containing an immunodominant T-cell epitope, and at least one TNF-alpha B-cell epitope. The substitution causes a significant change in the amino acid sequence of any one of the strands in the front beta-sheet, any of the connecting loops or any of the B', I or D strands in the back beta-sheet. The TNF-alpha analogues are used as vaccines for treatment or prevention of diseases associated with excessive release or activity of TNF-alpha, e-grheumatoid arthritis, Crohn's disease, ulcerative colitis, cancer of any sorth.

Sequence 158 AA;

. 0 Length 158; 0; Indels 63.4%; Score 118; DB 2; L 100.0%; Pred. No. 3.6e-09; ive 0; Mismatches 0; 63.4% Best Local Similarity 100.0 Matches 22, Conservative

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à Q RESULT 11 ABB07279

Ą. ABB07279 standard; protein; 158

ABB07279;

(first entry) 26-MAR-2002 Human TNF-alpha analogue TNF30-5.

TNF-alpha; pharmaceutical; vaccine; self-protein; tumour necrosis factor; cetylpyridinium chloride; immunisation; antiinflammatory; antirheumatic; antiarthritic; antiulcer; cytostatic; antidiabetic; antipsoriatic; antidasthmatic; immunomodulator; neuroprotective; osteopathic; human;

TNF30-5.

Homo sapiens.

WO200197837-A1.

27-DEC-2001.

20-JUN-2001; 2001WO-DK000431

21-JUN-2000; 2000DK-0000966

(FERR) FERRING BV.

Bouman MHEM; Olesen OF, Balchen T,

WPI; 2002-114542/15. N-PSDB; ABA94389.

Novel vaccine composition for prevention/treatment of self-protein-mediated pathology such as cancer, diabetes and asthma, comprises modified immunogenic self-protein and surfactant capable of acting solubilizer.

Claim 21; Page 42-43; 55pp; English.

The invention provides a pharmaceutical vaccine composition (1) for the prevention or treatment of a self-protein-mediated pathology. The composition comprises at least one modified immunogenic self-protein (selected from modified TNP-alpha proteins) and a surfactant capable of eaching as a solubitzer. (1) is useful for preventing or treating a self-protein-mediated pathology such as an inflammatory disease, rheumatoid arthritis, an inflammatory bowel disease (ulcerative colitis or Crohn's

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the specification
                                                                                                                                                             Sequence 750 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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20-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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ID AAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY92627-49 are mutant immunogenized human prostate specific membrane antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30). The immunogenic analogues of PSM can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor associated peptide
disease), cancer, cachexia, multiple sclerosis, diabetes, psoriasis, osteoporosis or asthma. (I) is useful for inducing autoantibodies to a self-protein such as TNF (tumour necrosis factor)-alpha in a human subject. (I) comprising cetylpyridinium chloride as a component is useful for immunisation of a human subject or for treatment of a human inflammatory disease. The present sequence represents a human TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalum I;
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               Prostate specific membrane antigen; immunogenized construct; mutant; vaccination; cytotoxic T-lymphocyte immunity; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope.
                                                                                                                                                                                                                                                                                            Mutant human prostate specific membrane antigen construct, hPSM1.1.
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leach D,
                                                                                                         Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune responses to weakly immunogenic, tumor as for the treatment of breast and prostate cancer.
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                         63.4%; Score 118; DB 5; I 100.0%; Pred. No. 3.6e-09; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haaning
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "foreign epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                           "foreign epitope'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nielsen KG,
                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                        133 FNNFTVSFWLRVPKVSASHLEG 154
                                                                                                                                                                                                                              AAY92627 standard; protein; 750 AA
                                                                                                                                                   1 FINETVSFWLRVPKVSASHLEG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouritsen S, Niels
irk P, Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-DK000525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DK-00001261
98US-0105011P
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "fore
32. .52
/label= P30
                                                                                                                                                                                                                                                                                                                                                                                                               /label= P2
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                               22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEBI-) M & B BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-349917/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birk P,
                                                                                                                     Local Similarity
                                                                analogue TNF30-5
                                                                                      Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200020027-A2
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1998;
                                                                                                                                                                                                                                                                       10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinaa L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gautam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing a
                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                   AAY92627;
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                 Matches
                                                                                                                                                                                                                     AAY92627
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human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producting cells (AFC8) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-1ymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the PA and/or at least 1 B-cell group derived from the foreign to the animal. Analogues of human PSM, human Her2 and human/murine PGR8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively. Note: This sequence was constructed the smoothing in the smoothing the stream of the symptom of the smoothing the stream of the smoothing that the smoothing the stream of the smoothing that the smoothing the smoothing that the smoothing the smoothing the smoothing that the smoothing that the smoothing the smoothing the smoothing the smoothing that the smoothing the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92627-49 are mutant immunogenized human prostate specific membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate specific membrane antigen; immunogenized construct; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant human prostate specific membrane antigen construct, hPSM1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination, cytotoxic T-lymphocyte immunity, breast cancer;
prostate cancer; cell-associated peptide antigen, foreign epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 117; DB 3; Length 750;
pred. No. 3e-08;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing immune responses to weakly immunogenic, tumor as
antigens for the treatment of breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24. .38
/label= P2
/note= "foreign epitope"
301. .321
/label= P30
/note= "foreign epitope"
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Birk P, Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FNNFTVSFWLRVPKVSASHLEGP 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 FNNFTVSFWLRVPKVSASHLETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92636 standard; protein; 750
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98US-0105011P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.7°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEBI-) M & E BIOTECH AS
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antigen (PSW) constructs, which contain foreign epitopes (P2 and/or P30).

The immunogenic analogues of PSM can be used in the claimed method as an autocative to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. The method is used for inducing immune responses against weakly immunogenic cell-associated peptide immune responses against weakly immunogenic cell-associated peptide thuman prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibrobast growth factor 80 (PGP80). The method comprises effecting simultaneous presentation by antigen (PSM), heregulin 2 (Her2) and/or simultaneous presentation by antigen producing cells (APC8) of the animals immune system of: (1) at least 1 acell group derived from the PA and/or at least 1 acell group derived from the PA and/or at least 1 acell group derived from the PA and/or at least 1 acell group which is foreign to the animal. Analogues of human PSM, human Her2 and produced CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to reat prostate, prosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoprotegerin ligand, OPGL, osteoprotegerin, osteoclastogenesis, tumour necrosis factor receptor; type II transmembrane protein, osteoclast differentiation; CSF-1, osteoclast activator; immune response; osteoporosis; bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An osteoprotegerin ligand/tetanus toxoid P30 epitope fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.9%; Score 117; DB 3; Length 750; llarity 75.8%; Pred. No. 3e-08; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "residues 158-255 of murine OPGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134. .188
/note= "residues 262-316 of murine OPGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FUNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .14
/note= "His tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84423 standard; protein; 188
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98US-0102896P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 750 AA;
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-1999;
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Peptide
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The present sequence represents fusion protein of murine osteoprotegerin cligand (OPGL) and tetamus toxoid P30 epitope. Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclast commendation is dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous OPGL is a potent osteoclast of inferentiation for the new protein combined with CSP-1. It is not capable of differentiation at the combined with the absence of CSF-1. OPGL is also inducing osteoclast differentiation in the absence of CSF-1. OPGL is also are civator of mature osteoclasts. The specification describes a method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at meniorating osteopoxosis or other diseases or conditions characterised by excessive bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲;
                                                                                                                                              In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multimeric protein; interleukin 5; ILS; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5; ILS; epitope; human; tetanus toxoid; chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.4%; Score 116; DB 3; Length 188; 82.1%; Pred. No. 8.6e-09; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hIL5-P2-P30-hIL5 (hIL5.35) fusion construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. .19
note= "Human IL5 leader peptide"
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/note= "Mature hIL5.35 protein"
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                                                                                                                                                                                                                                                   Example; Page 94-95; 110pp; English
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16-NOV-2001; 2001US-0331575P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2002; 2002WO-DK000764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
Halkier T, Haaning J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PHAR-) PHARMEXA AS.
(KLYS/) KLYSNER S.
(NIEL/) NIELSEN F S.
                                                              WPI; 2000-271444/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003042244-A2
                                                                                             N-PSDB; AAZ99970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 188 AA;
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric.
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Bratt T, Voldborg B, Mouritsen S;

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The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (IL5) and turnour necrosis factor alpha (TMF, TWRSIDha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in 2 near therapy. The present sequence is a fusion construct which comprises 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes 100 and P2. This sequence is used to illustrate the method of the invention
                                                                                                                                                                      New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                   Claim 20; Page 112-113; 196pp; English.
                                                                           Klysner S, Nielsen FS,
                                                                                                                WPI; 2003-449558/42.
N-PSDB; AAL61294.
(BRAT/) BRATT T.
(VOLD/) VOLDBORG B.
(MOUR/) MOURITSEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 285 AA;
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0; Gaps Query Match 62.4%; Score 116; DB 6; Length 285; Best Local Similarity 91.7%; Pred. No. 1.4e-08; Matches 22; Conservative 1; Mismatches 1; Indels 1 FUNETVSFWLRVPKVSASHLEGPS 24 à g

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Search completed: March 10, 2004, 09:12:10 Job time : 52.1984 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 10, 2004, 08:58:54; Search time 10.5837 Seconds

(without alignments)

309.015 Million cell updates/sec
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US-09-848-834A-10 score: 186 1 sharemeent bidevice surpropertings of	able:	d: 283366 segs, 96191526 residues	Total number of hits satisfying chosen parameters: 283366
Title: Perfect score:	sequence: Scoring table:	Searched:	Total number o

Total number of hits satisfying chosen parameters: Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_78:*
1: pir1:*
2: pir2:*
3: pir2:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	•	botulinum neurotox	rin pr		neurotoxin type F	neurotoxin type F	neurotoxin - Clost	bontoxilysin (EC 3	bontoxilysin (EC 3	non-proteolytic bo	gonadoliberin prec	probable transmemb	neurotoxin type E	botulinum neurotox	botulinum neurotox	hypothetical prote	botulinum neurotox	gonadoliberin prec	botulinum neurotox	botulinum neurotox	botulinum neurotox		probable alpha-amy	DNA-directed DNA p	rae	erin -	gonadoliberin - sh		nucleocapsid prote
SUMMARIES		, , , , , ,																												
SUMM	Ü	TCLTN	833411	RHRTG	548110	S48109	I40813	839791	BTCLAB	A48940	140631	RHMSG	T36589	848106	JH0256	821178	T01618	I40645	RHHUG	570582	546431	4	178541	B37837	T17202	S78196	RHPGG	RHSHG	151423	315
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	GOYG	112	62	61.5	61	61	61	61	59	58	28	57.5	57	vo	56.5	ဖ	56	56	54.5	4	54.5	4,	54	ന	53.5	53	52	52	52	52
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nonstructural prot	nonstructural proc	medaka-type gonado	cytochrome-c oxida	probable maturase	protein kinase (EC	probable myb-like	aconitase - Aquife	hypothetical prote	toxin, nontoxic co	botulinum neurotox	alpha galactosyltr	hypothetical prote	hypothetical prote	spheroidene monoox	ATP-binding casset
1 MINVUMC	1 MINUUM1	2 JC7393	2 S78195	2 S78197	2 S22441	2 T38197	2 F70453	2 T18627	2 JQ1467	2 S46430	2 T52082	2 T30273	2 T04726	2 S04401	2 JE0248
464	467	91	537	573	292	496	629	944	1196	1196	438	1450	432	591	836
28.0	28.0	27.7	27.7	27.7	27.4	27.4	27.4	27.4	27.4	27.4	27.2	27.2	26.9	26.9	26.9
52	52	51.5	51.5	51.5	51	51	51	51	51	51	50.5	50.5	50	0.50	20
30	31	32	33	3.4	in m	36	3.7	38	39	40	4	42	4.3	4	4.5

ALIGNMENTS

	RESULT 1
	tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
	N.Alternate names: tetanus neurotoxin
	C)Specials: closuring americans C.bate. 18: Mar-1988 #semience revision 31-Mar-1988 #text change 03-Jun-2002
	;
	R, Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel,
	BMBO (1.5, 2455-250.) 1986 A. Witle. Tetamis forin. orimary structure, expression in B. coli, and homology with bo
_	A25689; MUID:87053814; PMID:3536478
	A,Accession: A25689
	A;Molecule type: DNA A:molecule 1-1115 <fts< th=""></fts<>
	A. Cross-references: GB: X04436; NID: 940769; PIDN: CAA28033.1; PID: 940770
	R;Fairweather, N.F.; Lyness, V.A.
	Nucleic Acids Res. 14, 7809-7812, 1946 The first much and the first of
	A)ILLE: The Complete Nucleotide Sequence Of Technical Commission A) Reference number: A25/57; WUID:8704074; PMID:3774547
	A. A. A. S.
_	A; Molecule type: DNA
	A; Residues: 1-1315 <fai></fai>
	A; Cross references GB: NO6214; NID: 940//3; FIDN: CAAZSSSS, I; FID: 940//4
	A/EXPETIMENCE: BULGIN CHOSTI CHOSTI COSTINICASTI D. T.: Allen. G.: Thomson, R.O.
	A; Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in
	A; Reference number: A25194; MUID:86085672; PMID:3510187
	A;Accession: A25194
	A;Residues: 743-1315 <fa2></fa2>
	APACCESSION: DOLLOW WAS NOT A WAY OF A
	A.M. Carecure - (1720 - 1720 -
	R.Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
	1588-3593, 1989
	A, Title: Isolation, purification, and Characterization of Iragment b, the Nn-z-telmina
	AAACCESION: ABOUTS
	R. Demotz. S.: Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
	:
	A, Title: Delineation of several DR-restricted tetamus toxin T cell epitopes.
	A)Reference number: JSO98; MUID:89093918; FMID:2403303
	A; Contents: amuncatun; epitude region. R: Schiavo. G.: Benfenati, F.: Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B
	•
	A,Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteon
	A Reference number: SZ7125; MUID:93083293; FMID:153180/
_	A/concents: annotation

gonado

common precursor of

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A)Description: stimulates pituitary secretion of lutropin and follitropin
A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activiy
C;Superfamily: gonadoliberin
C;Keyncas: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-92/Product: progonadoliberin #status predicted <GN>
F;24-32/Product: gonadoliberin #status predicted <GN>
F;24-32/Product: prolactin release-inhibiting factor #status predicted <PIF>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross references: GB:M12579; NID:g204445; PIDN:AAA41263.1; PID:g204446
R;Maier, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
Cell. Mol. Neurobiol. 12, 447-454, 1992
A;Titler Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormon A;Reference number: A48410; MUID:93105480; PMID:1468115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs.

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CiSpecies: Clostridium botulinum

CiSpecies: Clostridium botulinum

CiSpecies: Clostridium botulinum

CiSpecies: 14-dul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

CiAccession: S48110

Ricampbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and special expecies number: S48103; MulD:94013372; PMID:8408542

A;Accession: S48110

A;Molecule type: DNA

A;Residues: 1-366 <CAM>
A;CAM>
A;CASS references: EMBL:X70821; NID:9407792; PIDN:CAA50152.1; PID:9407793

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: thymus
A;Note: sequence extracted from NCBI backbone (NCBIN:121082, NCBIP:121083)
C;Genetics:
                                                                     A;Coss-references: GB M31670; NID:g204447; PIDN:AAA41264.1; PID:g204448 R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H. Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986 A;A;tle: Isolation of the gene and hypothalamic cDNA for the common prect A;Reference number: A94090; MUID:86094338; PMID:2867548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mXNA
A;Residues: 1-92 <MAI>
A;Cross-references: GB:S50870; NID:g262059; PIDN:AAB24572.1; PID:g262060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61.5; DB 1; Length 92;
Pred. No. 0.14;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 2;
Pred. No. 0.76;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPKLMAAVVLLTVCLEGCSSQHWSYGLRP
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57.1%;
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1 Similarity 51.7%;
15; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-92 <ADE>
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                                                                                                                                                                                                                                                                                                                     A; Accession: B26173
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                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 2-31 < DEF>
C; Comment: The source of this protein was an extrachromosomal plasmid.
C; Comment: The source of this protein was an extrachromosomal plasmid.
C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B; Comment: Fragment D forms ion channels in a lipid bilayer. Fragment C binds to ganglic C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt C; Superfamily: tetanus toxin C; Superfamily: tetanus toxin C; Superfamily: tetanus toxin C; Seywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc C; Seywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc P; 24-1315/Product: tentoxylysin heavy chain (fragment B.C) #status predicted <TIL> F; 461-864/Domain: channel forming (fragment B) #status predicted <TXB> F; 565-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC> F; 233, 237/Binding site: zinc (His) #status predicted
F; 234/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doctulinum neurotoxin type F - Clostridium barati
C;Species: Clostridium barati
C;Species: Clostridium barati
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: 834411, 831860
R;Thompson, D.E.; Hutson, R.A.; Bast, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
R;Thompson, D.E.; Hutson, R.A.; Bast, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
R;Thompson, D.E.; Hutson, R.A.; Bast, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
A;Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin
A;Reference number: 833411; MUID:93252228; PMID:8486245
R,de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C. Eur. J. Blochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin. A;Reference number: S69348; MUID:95262688; PMID:7744050
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1268 <THO>
A;Cross-references: EMBL:X68262; NID:g49138; PIDN:CAA48329.1; PID:g49139
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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100.0%; Pred. No. 2e-07;
ive 0; Mismatches 0
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Pred. No. 2.2;
4; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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922 YONFSVSFWVRIPK 935
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A,Molecule type: protein
A,Residues: 867-880;1148-1217, Y',1219 <GIM>
A,Residues: 867-880;1148-1217, Y',1219 <GIM>
A,Experimental source: strain Hall
A,Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after
R;DasGupta, B.R.; Dekleva, M.L.
Bjochimie 72, 661-664, 1990
A;Tile: botulinum neurotoxin type A: sequence of amino acids at the N-terminus and ar
A,Reference number: A60025; MUID:91120847; PMID:2126206
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A;Cros-references: EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID:g40382
A;Cros-references: EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID:g40382
A;Experimental source: NCTC 2916
B;PUJita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin componen A;Reference number: S67988; MUID:96096783; PMID:8521962
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Astatus: preliminary
Astatus: Deliminary
Astatus: 1.12 ePUJ>
Astatus: 1.12 ePUJ>
Astatus: 1.12 ePUJ>
Astatus: 1.15 ePUJ>
Astatus: 1.15 emers, B.; DasGupta, B.R.
Biochem. Biophys. Res. Commun. 162, 1388-1395, 1989
Astitle: Characterization of botulinum type A neurotoxin gene: delineation of the N-te A;Reference number: A33401; MUID:89350959; PMID:2669749
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A; Residues: 1-1296 <BIN>
A; Residues: 1-1296 <BIN>
A; Residues: 1-1296 <BIN>
A; Cross-references: GB:M30196; NID:g144864; PIDN:AAA23262.1; PID:g144865
A; Cross-references: GB:M30196; NID:g14864; PIDN:AAA23262.1; PID:g144865
A; Experimental source: strain 62A, subtype A
B; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, Bur. J. Biochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotox A; Reference number: S09492; MUID:90235864; PMID:2185020
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NyAlternate names: botulinum neurotoxin type A
Cispecies: Clostridium botulinum
Cispecies: Clostridium botulinum
Cispecies: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 18-Jun-1999
Cibacession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
Ribint, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
Biol. Chem. 265, 9153-9158, 1990
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison
A;Reference number: A35294; WUID:90264400; PMID:2160960
                            A,Molecule_type: DNA
A,Residues: 1-1297 <CAM>
A,Cross-references: EMBL:X74162; NID:g441275; PIDN:CAA52275.1; PID:g441276
C,Superfamily: tetamus toxin
C,Keywords: neurotoxin
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R;Gimenez, J.A.; DasGupta, B.R.
Derocein Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, A;Reference number: A53884; MUID:94000342; PMID:8397793
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Pred. No. 3.1;
9; Mismatches
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Best Local Similarity 38.1%;
Matches 8; Conservative
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A; Residues: 1-35 <BET>
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CjSpecies: Clostridium botulinum
CjSpecies: Clostridium botulinum
CjSpecies: Oloct-1994 #sequence_revision Ol-Dec-1995 #text_change 16-Jul-1999
CjAccession: SJ3979!
RjCampbell, K.; Collins, M.D.; East, A.K.
Biochim. Biophys. Acra 1216, 487-491, 1993
AjTitle: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A, Reference number: SJ3791; MUID:94092745; PMID:8268233
A;Accession: SJ3791
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Date: 140813; S48109
R;Bast, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A;Reference number: 140644
                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-369 <CAM>
A;Cross-references: EMBL:X70820; NID:g407790; PIDN:CAA50151.1; PID:g407791
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Superfamily: tetanus toxin
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          neurotoxin type F - Clostridium botulinum (fragment)
C,Species: Clostridium botulinum
C,Bate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
C,Accession: S48109
E,Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A,Title: Gene probes for identification of the botulinal neurotoxin gene and sA,Reference number: S48103; MUID:94013372; PMID:8408542
A,Accession: S48109
A,Scatus: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: tetamus toxin
C;Keywords: neurotoxin
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Rolecule type: DNA
A, Residues: 1-1274 (*RES)
A, Crooss-references: GB:M92906; NID:g144866; PIDN:AAA23263.1; PID:g144867
R, Campbell, K.D.; Colling, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A, Title: Gene probes for identification of the botulinal neurotoxin gene A, Reference number: S48103; MUID:94013372; PMID:8408542
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Pred. No. 0.77;
5; Mismatches 1
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Pred. No. 3;
5; Mismatches
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57.1%;
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Similarity 57.1%;
8; Conservative
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930 YONFSISFWVRIPK 943
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297 YONFSISFWVRIPK 310
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non-proteolytic botulinum neurotoxin type B precursor - Clostridium botulinum (Species: Clostridium botulinum (Species: Clostridium botulinum (Species: Clostridium botulinum (Species: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 16-Jul-1999 (Spacession: 140631; 848103; 848104; 836015 R. Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.E. Curr. Microbiol. 28, 101-110, 1994 A.K.; Thompson, D.E. Ayītile: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulin A;Reference number: 140631; MUID:94122659; PMID:7764370
                                                                                                                                                                                                              A, Molecule type: mRNA
A, Residues: 1-313,'S', 315-451 «KUR»
A, Residues: 1-313,'S', 315-451 «KUR»
A, Experimental source: strain Okra
A, Note: Bequence extracted from NCBI backbone (NCBIP:109365)
R, DasGupta, B.R.; Datta, A.
Biochimie 70, 811-817, 1988
A, Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with
A, Reference number: S07155; MUID:89000987; PMID:3139097
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A;Mocaule type: protein
A;Mosidues: 442-459 <CGH3>
A;Mosidues: 442-459 <CGH3>
B;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.
Nature 599, 832-835, 1992
A;Hille: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteoly A;Reference number: S27125; MUID:93063293; PMID:1331807
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Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic syna
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C;Superfamily: tetanus toxin
C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
C;2-441/Product: bontoxilysin B light chain #status experimental <LGHT>
F;442-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>
F;230,234/Binding site: zinc (His) #status predicted
F;231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Title: Minimal essential domains specifying toxicity of the light chains of Reference number: A42871, MUID:92340509; PMID:1634516
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A; Residues: 442-463, R', 465-467 <DA2>
R; Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
Arch. Biochem. Biophys. 238, 544-548, 1985
A; Title: Partial amino acid sequences of botulinum meurotoxins types
A; Reference number: S07128; MUID:85197963; PMID:3888113
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A,Molecule type: DNA
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Pred. No. 8
                                                                                                                             1,Accession: A42871
1,Status: nucleic acid sequence not shown
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FLDFSVSFWIRIPK 936
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A,Residues: 2-29,'M',31-45 <DAS>
A,Accession: S08562
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Best Local Similarity 64.3
Matches 9; Conservative
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Molecule type: protein
Residues: 2-17 <SCH2>
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Molecule type: protein
Residues: 2-16 <SCH1>
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                A; Molecule type: protein
A; Residues: 2-6,445-453, X', 455-457 < DAS1>
R; Besdutes: 2-6,445-453, X', 455-457 < DAS1>
R; Besdutes: 2-6,445-453, X'; Niece, R.
Biochemistry 26, 4162, 1987.
Biochemistry 26, 4162, 1987.
Biochemistry 26, 4162, 1987.
A; Tille: Partial sequence of the light chain of botulinum neurotoxin type A.
A; Reference number: A27000
A; Molecule type: protein
A; Residues: 2-47 < CAS2>
B; Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
B; Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
A; Residues: 2-47 < CAS2>
B; Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
A; Residues: 2-47 < CAS2>
B; Binz, T.; Blasi, J.; Vapas E and A botulinal neurotoxins.
A; Reference number: A49708; MUID: 94124495; PMID: 8294407
A; Tille: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
C; Genetics:
A; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaption catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C; Superfamily: tecanus toxin
C; Genetics:
A; Description: catalyzes hydrolase; metalloproteinase; neurotoxin; transmembrane prote C; Superfamily: tecanus botto;
C; Superfamily: Lecanus botto;
C; Superfamily: Lecanus botto;
C; Superfamily: Lecanus botto;
C; Superfamily: Lecanus botto;
C; Superfamily: Silve bontoxilysin A light chain #status experimental < HVY>
F; 223, 227/Binding site: Zinc (His) #status predicted
F; 224/Active site: Glu #status predicted
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NyAlternate names: botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum neurotoxin 18-Nov-1994 #text_change 18-Jun-1999
C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A48840; S48105; S21575; A22871; S07155; S08562; S07128; S08574
B;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 58, 2345-2334, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the type A;Accession: A48840; MUID:92384550; PMID:1514783
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Residues: 1-1291 «WH2-
Residues: 1-1291 »WH2-
Residues: 1-1291 «WH2-
Residues: 1-1291 »WH2-
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A;Molecule type: DNA
A;Cross-references: 634-994 «CAM»
A;Experimental source: proteclytic type B, strain NCTC 7273
A;Experimental source: proteclytic type B, strain NCTC 7273
A;Experimental source: proteclytic type B, strain NCTC 7273
A;Experimental source: Droteclytic type B, strain NCTC 7273
A;Description: Parbial amino acid sequence of botulinum neurotoxin type B and comparisic A;Reference number: S21575
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A;Residues: 36-217, (3, 219-224, 'S', 226-246 <SZA>
A;Croserreferences: EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PID:g40384
A;Croserreferences: EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PID:g40384
R;Kurazono, H.; Mochida, S.; Binz, T.; Elsel, U.; Quanz, M.; Grebenstein, O.; Wernars,
J. Biol. Chem. 267, 14721-14729, 1992
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Pred. No. 5.9;
4; Mismatches 2; Indels
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Best Local Similarity 57.1%;
Matches 8; Conservative
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938 YENFSTSFWIRIPK 951
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16 LEGCSSQHWSYGLRP

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A.Residues: 1-567 cCAM>
A.Residues: 1-567 cCAM>
A.Cross-references: EMBL:X70818; NID:g407784; PIDN:CAA50149.1; PID:g407785
A.Note: the nuclectide sequence was submitted to the EMBL Data Library, January 1993
C.Superfamily: tetanus toxin
C.Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                   Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
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A;Experimental source: strain A3(2)
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C;Species: Clostridium botulinum
C;Species: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: 848106
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J; Cillin Microbiol. 31, 2255-2262, 1999
A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Reference number: S48106
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA.
                                                                                                                                                                             probable transmembrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Accession: T3689
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandre submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Accession: T36589
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Reference box and a coelicolor coelic
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C;Superfamily: Mycobacterium tuberculosis probable membrane protein Rv0051
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Best Local Similarity 50.0%; Pred. No. 4;
Matches 8; Conservative 3; Mismatches
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Pred. No. 3.3;
8; Mismatches
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Best Local Similarity 22.4%;
Matches 15; Conservative
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C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
C; Accession: A47578
R; Mason, A.U.; Hayflick, U.S.; Zoeller, R.T.; Young III, W.S.; Phillips, H.S.; Nikolics, Science 234, 1366-1371, 1986
A; Title: A deletion truncating the gonadotropin-releasing hormone gene is responsible for A; Reference number: A47578; MUID:87069928; PMID:3024317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A pescription: gonadoliberin stimulates pituitary secretion of lutropin and follitropin A; Note: gonadoliberin-associated protein may have prolactin release inhibiting activity S; Superfamily: gonadoliberin
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
P; 1-23/Domain: signal sequence #status predicted <SIG>P; 22-31/Product: gonadoliberin #status predicted <GIB>P; 35-90/Product: gonadoliberin-associated protein #status predicted <GAP>P; 22/Modified site: pyrolidone carboxylic acid (GIN) (in mature form) #status predicted P; 31/Modified site: amidated carboxyl end (GIY) (amide in mature form from following gIY)
A;Cross-references: EMBL:X71343; NID:g296148; PIDN:CAA50482.1; PID:g296149
R;Campbell, K.D.; Collins, M.D.; East, A.K.
C. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: $48103; MUID:94013372; PMID:8408542
A;Accession: $48103
                                                                                                                                                                                                                                                                        A,Status: preliminary, nucleic acid sequence not shown, translation not shown A,Status: preliminary, nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Molecule type: DNA A,Cross-references: EMBL:X70814; NID:g407778; PIDN:CAA50145.1; PID:g407779 A;Experimental source: non-proteclytic strain 2129B (Scott) A;Mote: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 A;Accession: 848104 A;Mote: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 A;Access-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781 A;Residues: 614-843, Tr',845, N',847-994 cCAM2> A;Across-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781 A;Experimental source: non-proteclytic strain Eklund 2B (Colworth 229) C;Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic G;Genetics: Dont/b C;Superfamily: tetanus toxin
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F;2-441/Product: botulinum neurotoxin type B light chain #status predicted <LGHT>
F;442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVN
F;230,234/Binding site: zinc (His) #status predicted
F;231/Active site: Glu #status predicted
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Pred. No. 8.1;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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A;Residues: 1-90 <MAS>
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Dotulinum neurotoxin type B precursor - Clostridium butyricum C;Species: Clostridium butyricum C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 16-Jul-1999 C;Accession: JHO256; 816145 R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R. A;Colet, Biophys. Res. Commun. 183, 107-113, 1992 A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum tyn A;Reference number: JHO256; MUID:92181428; PMID:1543481

7

Gaps

Length 90; Indels

DB 1;

Score 57.5; DB Pred. No. 0.51; 0; Mismatches

30.9%;

Query Match Best Local Similarity

Conservative

20 LEG-PSLHWSYGLRP 33

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Search completed: March 10, 2004, 09:16:46 Job time: 11.6425 secs
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 15-Oct-1999
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 15-Oct-1999
C;Accession: S21178; 848107; ÜH0257; B35294; A60027; S18<u>1</u>11
R;Whelan, S.M.; Blmore, M.J.; Bodsworth, N.J.; Akkinson, T.; Minton, N.P.
Eur. J. Biochem. 204, 657-667, 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin A;Reference number: S21178; MUID:92174922; PMID:1541280
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                                         A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-27, 'E', '29-1251 <POU>
A; Residues: 1-27, 'E', '29-1251 <POU>
A; Experimental source: strains ATCC 43181 and ATCC 43755
A; Experimental source: strains ATCC 43181 and ATCC 43755
A; Experimental source: strains ATCC 43181 and ATCC 43755
A; Fiblii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N.
J. Gen. Microbiol. 137, 519-525, 1991
A; Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxi
A; Reference number: S16145; MUID: 91237316; PMID: 2033376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: DNA A Molecule type: DNA A Molecule type: DNA Molecule type: DNA Molecule type: DNA Molecule type: 1-259, MV, 231-252 <FUJ>
A) Kresidues: 1-259, MV, 231-252 <FUJ>
A) Experimental source: Strain BL6340
A) Experimental source: Strain BL6340
C) Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release C) Comment: The heavy chain mediates the binding of toxin to cell receptors while the light C) Superfamily: tetanus toxin
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A; Residues: 1-176, "R', 178-197, C', 199-339; PIDN:CAA43999:1; PID:g40394
A; Experimental source: strain Beluga
R; Binz, T.; Kurazono, H; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
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Residues: 1-1252 (WHE>
Residues: 1-1252 (WHE>
Cross-references: EMBL:X62683; NID:g40397; PIDN:CAA44558.1; PID:g40398
Cross-references: EMBL:X62683; NID:g40397; PIDN:CAA44558.1; PID:g40398
Clampbell, K.D.; Collins, M.D.; East, A.K.
Clin. Microbiol. 31, 2255-2262, 1993
Tittle: Gene probes for identification of the botulinal neurotoxin gene and specific Reference number: S48103; MUID:94013372; PMID:8408542
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Pred. No. 13;
8; Mismatches
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Best Local Similarity 22.4%;
Matches 15; Conservative
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972 KLAFNYG 978
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A; Accession: JH0256
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A Molecule type: protein.

A) Residues: 420-47 < CIMP.

A) Residues: 420-47 < CIMP.

A) Residues: 420-47 < CIMP.

A) Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin C, Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit ne C, Comment: The heavy chain mediates the binding of toxin to cell receptors while the li C, Superfamily: tetanus toxin
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; MUID:90264400; PMID:2160960
A;Accession: B35294
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-176, 78', 178-252 <BIN>
A; Residues: 1-176, 78', 178-252 <BIN>
A; Experimental source: struction Beluga
R; Gimenez, J.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
A; Title: Borulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A; Title: Borulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A; Title: Borulbor: A60027; MUID:90344918; PMID:2116911
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22.4%;
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Q01886 cochliobolu
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10-OCT-2003 (Rel. 42, Last annotation update)
15-tanus toxin precursor (EC 3.4.24.68) (Tentoxylysin) [Contains:
15-tanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
chain (Tetanus toxin chain H)].
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MEDLINE-90201034; PubMed-2108021;
Krieglstein K., Henschen A., Weller U., Habermann E.;
"Arrangement of disulfide bridges and positions of sulfhydryl groups in tetanus toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O., "Cloning, mucleotide sequencing, and expression of tetanus toxin Leagment C in Escherichia coll.";
J. Bacteriol. 165:21-27(1986).
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Plasmid pE88, and Plasmid 75 Kbp.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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MEDLLIS=2245753; PubMed=12552129;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H. Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G.,
"The genome sequence of Clostridium tetani, the causative agent tetanus disease.";
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Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,

Weller U., Hudel M., Habermann E., Niemann H.;

"Tetanus toxin: primary structure, expression in E. coli, and

homology with botulinum toxins.";

EMBO J. 5:2495-2502(1986).
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WEDLINE=87040747; PubMed=3774547;
The complete nucleotide sequence of incleic Acids Res. 14:7809-7812(1986)
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MEDLINE=86085672; PubMed=3510187;
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292
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Match
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57.5
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Sax M.;
"Structure of the receptor binding fragment HC of tetanus
neurotoxin."
"Structure of the receptor binding fragment HC of tetanus
neurotoxin."
I "STRUCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPIRAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPERITASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
BOND OF SYNAPTOBREVIN-2.
--- CATALYIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
MEDLINE=97475217; PubMed=9334741;
Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identification of Substrate.

Middline=93063233; Pubmed=1331807;
Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.;
Tretanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.";
Nature 359:832-835(1992).
                                                                                                                                                                                                                                                                          identification AS ZINC-PROTEASE.
MEDILME=93010946; PubMed=1396558;
Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
Montecucco C.;
                                                                                       MEDLINE=9237649; PubMed=1935979;
Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;
"Limited proteolysis of tetanus toxin. Relation to activity and
identification of cleavage sites.";
Eur. J. Biochem. 202:41-51(1991).
Eur. J. Biochem. 188:39-45(1990)
                                                                PARTIAL SEQUENCE
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| Processor | Proc
               control of the Burden of the B
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InterPro; IPR002160; Kunitz_legume.
InterPro; IPR006025; Pept_M_Zn_BS.
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RESULT 3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@l8b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays an important role in the de novo pathway of purine nucleotide biosynthesis.
-!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rankin S., Li Z., Isberg R.R., "Macrophage induced genes of Legionella pneumophila: protection from reactive intermediates and solute imbalance during intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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FIGNOITE, PSOILS64, ADENYLOSUCCIN SYN 1; 1.

PROSITE; PSOOSI13, ADENYLOSUCCIN SYN 2; 1.

PROSITE; PSOOSI13, ADENYLOSUCCIN SYN 2; 1.

PUTINE BLOSYNCHESIS; LIGASE, GTP-binding, Metal-binding, Magnesium.

13 GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenylosuccinate.
-!- COFACTOR: Binds I magnesium ion per subunit (By similarity).
-!- PATHWAY: AMP biosynthesis; first committed step.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                              28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legionella pneumophila.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=446;
       Length 1314;
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                                                                   0; Indels
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Query Match
60.2%; Score 112; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 YHNFVLTQYFKQPAVDLESLLGESLQWAEELRP 200
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                                                                                                                                                                                                                                                                                                                                                                     PRT; 431 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF480918; AAM00648.1; -. HAMAP; MF 00011; -; 1.
InterPro; IPR001114; Asucc synthtase.
Pfam; PF00709; Adenylsucc synt; 1.
ProDom; PD001188; Asucc_synthtase; 1.
                                                                                                                                                                                             946 FNNFTVSFWLRVPKVSASHLE 966
                                                                                                                                    1 FNNFTVSFWLRVPKVSASHLE 21
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                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     PURA LEGPN
QBRNM2;
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                                                            01-APR-1988 [Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
Luteinizing hormore-releasing hormone I) (Gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-86094338; PubMed=2867548;
Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
"Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat.";
                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthería; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
MADINNE=28149087; PubMed=3547652;
Adelnan J.P., Bond C.T., Douglass J., Herbert E.;
"Two mammalian genes transcribed from opposite strands of the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89384661; PubMed=2476669;
Bond C.T., Hayflick J.S., Seeburg P.H., Adelman J.P.;
"The rat gonadotropin-releasing hormone: SH locus: structure and

    -!- FUNCTION: Stimulates the secretion of gonadotropins; it stitus secretion of both luteinizing and follicle-stimulating

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93105480; PubMed=1468115; Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E.; Maroyces a mRNA that is identical to hypothalamic lutefinizing hormone releasing hormone mRNA."; Cell. Mol. Neurobiol. 12:447-454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION; Secreted.
-!- TISSUE SPECIFICITY: Central nervous system.
-!- SIMILARITY: Belongs to the GnRH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothalamic expression.";
Mol. Endocrinol. 3:1257-1262(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -, NOT ANNOTATED CDS.
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EMBL, M1579; AAA41264.1; --
EMBL, M15527; AAA41241.1; ALT_SEQ.
EMBL, M15529; AAA4134.1; --
EMBL, M15529; AAA4139.1; --
EMBL, M15529; AAA4139.1; --
                                 01-APR-1988 (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 235:1514-1517(1987).
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                                                                                                                                                                                                                                                                               GNRH1 OR GNRH.
DARANA DA
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OCCUPATION
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-!-FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
Pfam; PF00446; GDRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJUE=94013372; PubMed=9408542; Campbell K., East A.K., Collins M.D.; Gampbell K., East A.K., Collins M.D.; Gampbell K., East A.K., Collins M.D.; Gampbell K., Esst A.K., Collins M.D.; Gampellins for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, B, and F."; J. Clin, Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bast A.K., Collins M.D., "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nouroxic component in nonproteolytic Clostridium botulinum type F."; Curr. Microbiol. 29:69-77(1994).
                                                                                                                                                                                                                      Gaps
                                                                               PROGONADOLIBERIN I.
GONADOLIBERIN B.
PROLACTIN RELEASE-INHIBITING FACTOR I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                           PYRECIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
494B5C64DA8A3EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 2338;
MEDLINE=93012902; PubMed=1398040;
Bast A.K., Richardson P.T., Allaway D., Collins M.D.,
Roberts T.A., Thompson D.E.,
"Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.";
                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                           01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Boculinum neuroticxin type F precursor (EC 3.4.24.69) (BONT/F)
(Bontoxilysin F).
                                                                                                                                                                                          Score 61.5; DB 1; Length 92;
Pred. No. 0.076;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                               12 VPKVSAS-----HLEG-PSLHWSYGLRP 33
                                                                                                                                                                                                                                                                 4 IPKLMAAVVLLTVCLEGCSSQHWSYGLRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEMS Microbiol. Lett. 75:225-230(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF SUBSTRATE.
MEDLINE=94230352; PubMed=8175689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
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                                                                                                                                                                       92 AA; 10500 MW;
                                                                                                                                                                                               Query Match
Best Local Similarity 51.7%;
Matches 15; Conservative
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SEQUENCE OF 1-64 FROM N.A.
                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                      BXF CLOBO
                                                                                   CHAIN
PEPTIDE
PEPTIDE
ACT_SITE
                                                                                                                                                                       SEQUENCE
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AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSISYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERTIBASE THAT CARLIZES THE HYDROLYSIS OF THE SHGIN-|-LYS-59 BOND OF SYNAPTOREVINS-1 AND -2.

CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocycosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -1- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain partial the heavy chain activity.

While the N- and C-terminal of the heavy chain mediate channel CC while the North Cordinors of SUBCELLULAR LOCATION: Secreted Activally.

CC -1- SUBCELLULAR LOCATION: Secreted CC -1- SUBCELLULAR LOCATION: Types A, B, Cl, D, E, R, and G. -1- SUBCELLULAR LOCATION: Secreted CC -1- SUBCELLULAR LOCATION: Types A, B, Cl, D, E, R, and G. -1- SUBCELLULAR LOCATION: SECRETED CC -1- SUBCELLULAR LOCATION: SECRETED CC -1- SUBCELLULAR LOCATION: Types A, B, Cl, D, E, R, and G. -1- SUBCELLULAR LOCATION: SECRETED CC -1- SUBCELLULAR LOCATION: Types A, B, Cl, D, E, R, CL, D, E, R, CL, D, E, R, CL, D, E, R, CL, D,
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R InterPro; IPR002606; Kunitz_legume.

R InterPro; IPR002606; Fept.M_Zn=18.

R InterPro; IPR002605; Peptidase_MZ;

R InterPro; IPR002605; Peptidase_MZ;

R PRINTS; PR00196; BONTOXILYSIN.

R PROSITE; PR00196; BONTOXILYSIN; 1.

R PROSITE; PR00142; ZINC_PROTEASE; 1.

R PROSITE; PR00142; ZINC_PROTEASE; 1.

R PROSITE; PR00142; ZINC_CRAPASE; 1.

T CHAIN

WENTAL

T ACT SITE 228 228 BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.

T ACT SITE 228 228 BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.

T ACT SITE 228 ZINC (CATALYTIC) (BY SIMILARITY).

T DISULED 429 445 INTERCHAIN (PROBABLE).

O SEQUENCE 1274 AA; 146709 MW; 5899756A7438B921 CRC64;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurocoxin type G precursor (EC 3.4.24.69) (BONT/G)
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EMBL; 873876; AAC60475.1; --
EMBL; X70820; CAAS0151.1; --
EMBL; X70816; CAAS0147.1; --
PIR; 140813; 140813.
PIR; 548109; A84109.
HSSP; P10845; 3BTA.
MEROPS; M27.002; --
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Matches 8; Conserv
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Q60393;
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28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
(Bontoxilysin A) (BOTOX) (Contains: Botulinum neurotoxin A, light-chain; Botulinum neurotoxin A, heavy-chain).
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MEDLINE=91120847; PubMed=2126206;
Dasgupta B.R., Dekleva M.L.,
"Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site.";
Biochimie 72:661-664(1990).
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MEDLINE=96096783; PubMed=8521962;
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MEDLINE=84178501; PubMed=6370252;
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                                                                                                                                                                                                                                                            STRAIN=NCTC 2916;
MEDLINE=90235864; PubMed=2185020;
                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 189:73-81(1990).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=1491;
                                                                                                                                                                      Clostridium.
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                                                                              STRAIN=113 / 30;
MEDLINE=94092745; PubMed=8268233;
MEDLINE=94092745; PubMed=8268233;
MEDLINE=94092745; PubMed=8268233;
Campbell K., Collins M.D., Bast A.K.;
"Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium argentinense) type G neurotoxin: genealogical comparison with other clostridial neurotoxins.";
Biochim. Biophys. Acta 1216;487-491 (1993).
FINCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES. IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPIRAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS. NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                          --- CATALTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

--- CORACTOR: Binds 1 zinc ion per subunit (By similarity).

--- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N - and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.

--- SUBCELLULAR LOCATION: Secreted (By similarity).

--- MISCELLANSOUS: There are seven antigenically distinct forms of botulinum neurocoxin: Types A, B, Ci, D, E, F, and G.
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BOTULINUM NEUROTOXIN G, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
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ZINC (CATALYTIC) (BY SIMILARITY)
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MEROPS; M27.002; --

InterPro; IPR003160; Kunitz_legume.

InterPro; IPR003160; Kunitz_legume.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR00135; Peptidase_M27;

Refan; PF01742; Peptidase_M27; I.

R PRINTS; PR00760; BONTOXILYSIN.

R PRODM; PD00143; ZINC_PROTEASE; I.

RPOSITE; PS00142; ZINC_PROTEASE; I.

Neurocxin; Hydrolase; Metalloprotease; Zinc.

BY SINILARITY.
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FDNFSINFWVRTPKYNNNDIQ 949
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                       NCBI_TaxID=1491;
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Description T. Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
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Biochem, Biophys. Res. Commun. 162:1388-1395(1989).
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MEDINE=97016817; PubMed=8861443;
MEDINE=97016817; PubMed=8861443;
Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
int. J. Syst. Bacteriol. 46:1105-1112(1996).
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Binz B., Kuarzono H., Wille M., Frevent J., Wernars K., Niemann H.;
Binz B., Kuarzono et of botulinum neurotoxin type A and comparison
"The complete sequence of botulinum neurotoxin type A and comparison
with other clostridial neurotoxins";
J. Biol. Chem. 265:9153-9158(1990).
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Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae,
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REPURNES OF 444-644 AND 872-895.

REPURNES OF 444-644 AND 872-895.

REPURNES OF 444-644 AND 872-895.

REPURNES OF 444-645.

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NOTE=Issue 19 of February 2002;
WWW="http://www.expasy.org/spotlight/articles/sptlt019.html".

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                           BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
ZINC (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E->A: DRASTIC DECREASE IN ENZYMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVITY.
F->A: DECREASES ENZYMATIC ACTIVITY.
Y->A: DECREASES ENZYMATIC ACTIVITY.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P -> Q (IN REF. 1).
E -> P (IN REF. 9).
T -> L (IN REF. 8).
S -> K (IN REF. 8).
Ww, 858342F754862579 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             (CATALYTIC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59;
Pred. No. 3
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                                                                                                                                                                                                                             InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR002160; Kunitz legume.
InterPro; IPR006025; Pept_M_Zn_BS.
InterPro; IPR000395; Peptidase_M27.
Pfam; PF01742; Peptidase_M27; I.
PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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EMBL, M30196; AAA23262.1; --
EMBL; X92073; CAA63551.1; --
EMBL, D67030; BAA11051.1; --
EMBL, MX7882; AAA23269.1; --
PIR; A35294; BRCLAB.
PDB; 3BTA, 01-OCT-99.
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937 YENFSTSFWIRIPK 950
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875
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Q00496;
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VARIANT
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The following in the first state of the control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3] SEQUENCE OF 1-251 FROM N.A. NEDLINE=90264400; PubMed=2160960; MEDLINE=90264400; PubMed=2160960; Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.; The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins..., with other 265:9153-9158(1990)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.
Jahn R., Niemann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J.,
Benfenati F., Wilson M.C., Montecucco C.;
Boculinum neurotoxins serotypes A and E cleave SNAP-25 at distinct
COOR-terminal peptide bonds.";
FEBS Lett. 335:99-103 (1993).
                                              STRAIN=Beluga;
MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-13.

SEDILINE-88197963; PubMed=2888113;
Schnidt J.J., Sathyamcorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=90344918; PubMed=2116911; Gimenez J.A., Dasgupta B.R., Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the site trypein nicks and homology with tetanus
                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arch. Biochem. Biophys. 238:544-548(1985).
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MEDLINE=94063091; PubMed=8243676;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bur. J. Biochem. 204:657-667(1992)
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MEDLINE=92384550; PubMed=1514783;
Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
Minton N.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN E, HEAYY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
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Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Appl. Environ. Microbiol. 58:2345-2354(1992).
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InterPro; IPR006160; Kunitz_legume.
InterPro; IPR006025; Pept_MZ_nBs.
InterPro; IPR006025; Pept_MZ_nBs.
Pfam; PF01742; Peptidase_MZ7; I.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Bontoxilysin; I.
PROSTIE; PS00142; ZINC PROTEASE; I.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
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MW; D9FCE26DDA041EB4 CRC64;
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C -> S (IN REF. 2 AND 3).
R -> A (IN REF. 2).
F -> L (IN REF. 2).
F -> LQ (IN REF. 2).
R -> A (IN REF. 2).
N -> NN (IN REF. 2).
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966 966
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1250 AA; 143712 M
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ses 13; Conservative
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MEROPS; M27.002;
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                                                                                      Campbell K., East A.K., Collins M.D.; "Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                       MEDLINE=53054694; PubMed=1429690;
Schlavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;
"Boculinum neurotoxins are zinc proteins.";
J. Biol. Chem. 267:23479-23483(1992).
                                                                                                                                                                                                                                                                     Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.; "Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                         SEQUENCE OF 35-245 FROM N.A. STRAIN=NOTC 7273, SZADO E.A., Pemberton J.M., Desmarchelier P.M.; Syabo E.A., Pemberton J.M., EMBL/GenBank/DDBJ databases. Submitted (AFR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        Arch. Biochem. Biophys. 238:544-548(1985)
                                                                    STRAIN=NCTC 7273;
MEDLINE=94013372; Pubmed=8408542;
                                                                                                                                                                     MEDLINE=89000987; PubMed=3139097;
                                                                                                                                                                                                                                                              MEDLINE=85197963; PubMed=3888113;
                                                                                                                                                                                                                                                                                                                               IDENTIFICATION AS ZINC-PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M81186; AAA23211.1; -.
EMBL; Z11934; CAA77991.1; -.
EMBL; X70817; CAA50148.1; -.
                                                                                                                                              SEQUENCE OF 1-44 AND 441-466.
STRAIN=657;
                                                       SEQUENCE OF 633-993 FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE OF 1-16 AND 441-458.
                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF SUBSTRATE
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01-07N-1990 (Rel. 13, Created)
01-07N-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prognandoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GNRH I) (Luliberin I); Prolactin release-inhibiting factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gonadotropins; it stimulates follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=87069928; PubMed=3024317;
MEDLINE=87069928; PubMed=3024317;
MEDLINE=87069928; PubMed=3024317;
Phillips H.S., Mikolick J.S., Seeburg P.H.;
Phillips H.S., Mikolick K., Seeburg P.H.;
"A deletion truncating the gonadotropin-releasing hormone gene is responsible for hypogonadism in the hpg mouse.";
science 2341366-1371(1986).
---- FUNCTION: Stimulates the secretion of gonadotropins; it stimulate secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZING (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom, PD001963; Bontoxilysin; 1.
PROSITE, PS00142; ZINC PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 1; Length 1290;
Pred. No. 4.1;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> M (IN REF. 4).
R -> G (IN REF. 2).
A -> S (IN REF. 2).
S -> R (IN REF. 4).
Mw; D21746E2C024DF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the GnRH family.
                                                                                                                                                                                                                                                                                                               InterPro; IPR008985; Cona like_lec_g1
InterPro; IPR002160; Kunitz_legume.
InterPro; IPR006025; Pept M_Zn_BS.
InterPro; IPR000395; Peptidase M27.
PEam; PP01742; Peptidase M27; I.
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01742; Peptidase M27;
PRINTS; PR00760; BONTOXILYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.2%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150670
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922 FLDFSVSFWIRIPK 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                     PDB, IFQH, 06-DEC-00
PDB, IG9A, 13-NOV-02
PDB, IG9B, 13-NOV-02
PDB, IG9C, 13-NOV-02
PDB, IG9D, 13-NOV-02
PDB, ILE, 21-NOV-02
PDB, ILE, 21-NOV-02
PDB, ILE, 21-NOV-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 40
A48940; A48940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNRH1 OR GNRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GONI MOUSE
P13562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
METAL
ACT SITE
METAL
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GON1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
PIR;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
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GNRH1 OR GNRH
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                                                                             Query Match
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                                                                                                                                                                                                                                                              GON1 RAI
Q90Y63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African horse sickness virus 6 (AHSV-6) (African horse sickness virus
                                                                                                                                                                                                                                                                                residues; Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9827831; PubMed=9617769;
Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;

Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;

Virus Res. 53:53-73(1998).

-!- FINCTION: THE VIRUS PARTICLE OUTER CAPSID. IT IS THE MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.

-!- SIMILARITY: Belongs to the recoviruses VP2 protein family.
                                                                                                                                                                                                                                                                                                                                               GONADOLIBERIN I.
PROLACTIN RELEASE-INHIBITING FACTOR I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-32 PROVIDE AMIDE GROUP).
1C0766FA4826E4D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.5; DB 1;
Pred. No. 0.27;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                 PROGONADOLIBERIN I.
                                                                                                                                                               PIR; A47578; RHMSG.
MGD; MGI:95789; Gnrh.
InterPro; IPR002012; GnRH.
InterPro; IPR004079; GonadoliberinI.
Pfam; PF00446; GnRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
CREAVAGE on pair of basic residues; Hormone; Ar
Placenta; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VP2 AHSV6 STANDARD; PRT; 1051 AA. 071024.19
071024.1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
52 OR 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF021235; AAC40994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 22
31
10337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%;
80.0%;
                                                                                                                                               EMBL; M14872; AAA37717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LEGCSSOHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LEG-PSLHWSYGLRP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12, Conservative
                                                                                                                                                                                                                                                                                                                                   33
34
24
24
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31
90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (serotype 6))
                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
PEPTIDE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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VP2_AHSV6
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005183; F:luteinizing hormone-releasing factor activity; NAS.
GO; GO:00005183; F:luteinizing hormone-releasing factor activity; NAS.
GO; GO:0000755; P:hormone mediated signaling; NAS.
GO; GO:000003; P:reproduction; NAS.
InterPro; IPR004012; GRRH.
InterPro; IPR004012; GRRH.
PF00446; GRRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prognadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
Cluteinizing hormone releasing hormone I) (Gonadotropin releasing hormone I) (Gonadotropin releasing hormone I) (GARH I) (Luliberin I); GRRH-associated peptide I (GAPL)].
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of cDNAs encoding the GRH1 and GRH2 precursors from bullfrog (Rana catesbelana).";
J. Bxp. 2col. 289:190-2001(2001).
-!- FUNCTION: Stimulates the secretion of gonadotropins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBCELDULAR LOCATION: Secreted.
-!- SUBCELDULAR LOCATIONY: Forebrain.
-!- TISSUB SPECIFICITY: Forebrain.
-!- DEVELOPMENTAL STAGE: Expressed at significantly higher levels during post-breeding. Not expressed in pituitary.
-!- SIMILARITY: Belongs to the GRRH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
YCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage on pair of basic residues, Hormone, Amidation, Signal, Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNRH-ASSOCIATED PEPTIDE I (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Forebrain;
MEDILINE=21102951; PubMed=11170016;
Wang Li, Yoo M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J.,
Kwon H.B.;
                                                                                                                                                            Length 1051;
                                                                                                                                                                                                                               Indels
                                                                                               1051 AA; 122326 MW; 2B04DB9E389F4B5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGONADOLIBERIN I. GONADOLIBERIN I.
                                                                                                                                                            30.6%; Score 57; DB 1; 47.6%; Pred. No. 4.6; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                          636 FSKRFVSYWYRVEKITTKHLE 656
                                                                                                                                                                                                                                                                                                   1 FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
InterPro; IPR001742; Orbi_VP2.
Pfam; PR00898; Orbi_VP2; I.
Coat protein.
SEQUENCE 1051 AA; 122336 MW
                                                                                                                                                                                                                                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                   Local Similarity
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MEDLINE=94143603; PubMed=8310180;
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Q45894; P77780;
28-FEB-2003 (Rel. 41, Created)
                                                                EMBL; X62088; CAA43998.1; -. EMBL; X53180; CAA37321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        30.4%;
22.4%;
                                                                                                                                                                                                                                                                                                                                                                            143265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FUNFTVSFWLRVP---
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 22.4
nes 15; Conservative
                                                                                          PIR; JH0256; JH0256.
HSSP; P10845; 3BTA.
MEROPS; M27.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::||
971 KLAFNYG 977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                       METAL
ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gimenez J., Foley J., Dasgupta B.R.; Gimenez J., Foley J., Dasgupta B.R.; Neurotoxin type E from Clostridium botulinum and C. butyricum; partial sequence and comparison."; FASEB J. 2:41750-41750 (1988).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES. IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOPERPIDASE.

CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobravins, SNAP25 or syntaxin. No detected action on small molecule substrates.

COPACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BL6340;
MEDLINE=912331316;
MEDLINE=912331316;
MITAREARM T., Indoh T., Tsuzuki K.,
Yokosawa N., Kimura K., Murakami T., Indoh T., Tsuzuki K.,
Yokosawa N., Yashiki T., Oguma K.;
"Cloning of a DNA fragment encoding the 5'-terminus of the botulinum
"Cloning of a DNA fragment encoding the 5'-terminus of the botulinum
"Cloning of a DNA fragment From Clostridium butyricum strain BL6340.";
J. Gen. Microbiol. 137:519-525(1991).
 AMIDATION (G-35 PROVIDE AMIDE GROUP) (BY
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 41181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            formation and toxin binding, respectively.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: There seeven antigenically distinct forms botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
-!- SIMILARITY: Belongs to peptidase family M27.
                                                                                                                                                                                                                                                                                                                Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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س
                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-BUL-1993 (Rel. 41, Last amoutation update)
Botulinum neurotoxin type E precursor (BC 3.4.24.69) (BONT/E)
                                                         90;
                                                                                    Indels
                                                       Score 56.5; DB 1; Length
Pred, No. 0.38;
                  SIMILARITY).
317203B4E3DA2FE7 CRC64;
                                                                                    6
                                                                                                                                                                                                                PRT; 1250 AA
                                                                                    4; Mismatches
                                                                                                                                 5 TVSFWLRVPKVSASH-LEGPSLHWSYGLRP 33
                               10291 MW;
                                                         30.4%;
ilarity 46.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE OF 1-251 FROM N.A.
                                                                                                                                                                                                              STANDARD;
    34
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-48.
                               90 AA;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1492;
                                                                                                                                                                                                                                                                                                   Bontoxilysin E)
    34
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                                                          Query Match
Best Local Simil
Matches 14; (
                                                                                                                                                                                                                 CLOBU
                                 SEQUENCE
      MOD_RES
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=97016817; PubMed=8863443;
East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteclytic Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A, light-chain; Botulinum neurotoxin A, heavy-chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Willems A., East A.K., Lawson P.A., Collins M.D.; Sequence of the gene coding for the neurotoxin of Clostridium bendinner type A sassolated with infant botulism: comparison with other clostridial neurotoxins."; Res. Microbiol 144:547-556(1993).
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Bacceria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; PR008985; ConA like_lec_gl.

InterPro; PR008985; ConA like_lec_gl.

InterPro; PR0002160; KuniEr_legume.

InterPro; PR0002160; Pept M Zn Bs.

InterPro; PR01042; Peptidase_M27.

R PRINTS; PR001767; PR001767; PR001767; PR001767; PR001763; BONTOXILYBIN.

R PROSITE; PS00142; ZINC_PR0TRASE; 1.

Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.

I INIT MET 1 421 BOTULINIM NEUROMOVIN P. PROPERTY P. PROFESTIVE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALXTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
K -> M (IN REF. 2).
K -> M (1N REF. 2).
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HEAVY-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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potulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

I. 1. 5. Syst. Bacteriol. 46:1105-112(1996)

I. 1. FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated andocytosis.

The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus and the cytosol. After transported the light chain (E) hydrolyzes the 197-Gln-[-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure (By similarity).

C. -CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neurotrosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).

C. HISCELLANBOUS: There are seven antigenically distinct forms of control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration the tween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
ZINC (CATALYIC) (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 1; Length 1295;
Pred. No. 7.9;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149279 MW; 5DA04A13D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 01, Created)
(Rel. 07, Last sequence update)
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50.0%;
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1234 127
626 64
655 67
1295 AA;
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7; Conservat
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ID GON1_HUMAN
AC PO1148;
DT 21-JUL-1986 (
DT 01-APR-1989 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 23:373-373 (1999).
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lander E.S.; "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
                                                                                                                                                                                                                                                                                                                                                                 SECTENCE FROM N.A.
MEDLINE=86094338; PubMed=2867548;
Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
"Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat.";
Proc. Natl. Acad. Sci. U.S.A. 83:179-183 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT SER-16.
MEDIATE-99318093, PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-8936682; PubMed=2671939;
Hayflick J.S., Adelman J.P., Seeburg P.H.;
"The complete nucleotide sequence of the human gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLUIAR LOCATION: Secreted.
-!- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
Lutrepulse or Lutrelef (Ferring Pharmaceuticals) and Relisorm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT SER-16.
MEDLINE=85012739; PubMed=6090951;
Seeburg P. H., Adelman J.P.;
"Characterization of cDNA for precursor of human luteinizing hormone
28-FEB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precureor [Contains: Ganadoliberin I (LH-RH I)
[Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
hormone I) (GRH I) (Luliberin I) (Gonadorelin); GRRH-associated
                                                                                                   GNÄHI OR GNRH OR LHRH.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 24-33.
MEDLINE-83126573; PubMed=6760865;
Tan L., Rousseau P.;
"The chemical identity of the immunoreactive LHRH-like peptide biosynthesized in the human placenta.";
Biochem. Biophys. Res. Commun. 109:1061-1071(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: Belongs to the GnRH family.
                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 17:6403-6403(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             releasing hormone.";
Nature 311:666-668(1984).
                                                                                                                                                                   Mammalia, Euther
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lander E.S.;
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Gaps

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PRINTS; PROIS4; MONADOLIBRNI.
PROSITE; PS06473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Pharmaceutical; Signal; Polymorphism;
Pyrrolidone carboxylic acid.
SIGNAL
1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=90370487; PubMed=2204031; MEDLINE=90370487; PubMed=2204031; Hauser D., Eklund M.W., Kurazona H., Binz T., Niemann H., Gill D.M., Boquet P., Popoff M.N.; M.R.; "Nucleotide sequence of Clostridium botulinum C1 neurotoxin."; Nucleotide Rege 18:4924-4924(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                 GO; GO:0006625; C:soluble fraction; TAS.
GO; GO:0005628; F:luteinizing hormone-releasing factor activity; TAS.
GO; GO:0005267; P:cell-cell signaling; TAS.
GO; GO:000725; P:development; TAS.
GO; GO:0007165; P:negative regulation of cell proliferation; TAS.
InterPro; IPR002012; GRRH.
InterPro; IPR004079; GonadoliberinI.
                                                                                                                                                                                                                                                                                                           PROGONADOLIBERIN I.
GONADOLIBERIN I.
GONADOLIBERIN I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRINI-Type C Stockholm / C-ST;
MEDLINE-91024998; Pubmed-2222445;
Kimura K., Fujii N., Tsuzuki K., Muraxami T., Indoh T.,
Yokosawa N., Takeshi K., Syuto B., Oguma K.;
The complete nucleotide sequence of the gene coding for botulinum
type C1 toxin in the C-ST phage genome.";
Bjochem. Biophys. Res. Commun. 171:1304-1311(1990).
                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLLC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
W -> S (in dbSNP:6185).
FTTA=VAR 013943.
30A72221E076FA79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurotoxin type Cl precursor (EC 3.4.24.69) (BONT/Cl)
(Bontcxilyain Cl).
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; DB 1; Length 92; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2-25.
STRAIN=TYPE C Stockholm / C-ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA; 10380 MW;
EMBL; X01059; CAA25526.1; -. EMBL; M12578; AAA35916.1; -. EMBL; X15215; CAA33285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LEG-PSLHWSYGLRP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 VEGCSSOHWSYGLRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                         HGNC:4419; GNRH1.
                            EMBL; X15215; CAA3
PIR; S05308; RHHUG
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NCBI_TaxID=1491;
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SEQUENCE OF
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                                                         Genew;
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Oguma K.; "Establishment of a monoclonal antibody recognizing an antigenic site common to Clostridium botulinum type B, Cl, D, and E toxins and

tetanus toxin."; Infect. Immun. 56:898-902(1988).

Fauzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,

MEDLINE=88153072; PubMed=2450068;

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NEUTIFICATION OF SUBSTRATE.

WEDLINE=94038966; PubMed=7901002;

MEDLINE=94038966; PubMed=7901002;

MEDLINE=94038966; PubMed=7901002;

Blasi J., Chapman E. R., Yamasaki S., Binz T., Niemann H., Jahn R.;

Blasi J., Chapman E. R., Yamasaki S., Binz T., Niemann H., Jahn R.;

Blasi J., Chapman E. R., Yamasaki S., Binz T., Niemann H., Jahn R.;

Relaving HPC-1/Fyntaxin.";

RELEASE 19818(1993).

C. 1- GAPLINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROCRADE TRANSFORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INTIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

RNDOPEPTIDASE THAT CLEAVES SYNTAXIN.

C. CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C. CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

C. I. SUBUNIT: Disulfide-linked heterodimer of a light chain (H) The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.

C. I. SUBCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.

C. I. MISCELLANBOUS: BOTULINUM WHICH CARRY THE APPROPRIATE PARTER P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 448 | BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN. |
449 | 1290 | ZINC (CATALTIC) (BY SIMILARITY). |
228 | 228 | ZINC (CATALTIC) (BY SIMILARITY). |
232 | 232 | ZINC (CATALTYC) (BY SIMILARITY). |
436 | 452 | INTERCHAIN (PROBABLE). |
84 | P -> T (IN REF. 2). |
1290 Aa; 148734 Mw; 71FBE379F97129E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMBL; X66433; CAA470600.1; -

R EMBL; X72793; CAA470600.1; -

R EMBL; X72793; CAA47060.1; -

R EMBL; X72793; CAA47060.1; -

R EMBL; X62369; CAA44263.1; -

R EMBL; X62369; CAA44263.1; -

R EMBL; X62369; CAA44263.1; -

R EMPL; X62369; CAA44263.1; -

R EMPL; M27002; -

R InterPro; IPR000405; Peptidase M27.

R InterPro; IPR000405; Peptidase M37.

R RINTS; RR00760; BONTOXILIYSIN.

R PROSITE; PS00142; ZINC PROTEASE; 1.

R ROSITE; PS00142; ZINC PROTEASE; 1.

R Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.

T INIT MT 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to peptidase family M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%; Score 54.5; D
30.8%; Pred. No. 13;
ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 12, Conserv
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Search completed: March 10, 2004, 09:13:53 Job time: 7.2179 secs

Sequence Sequence Sequence 1

Sequence 3 Sequence 5 Sequence 5 Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 6

Sequence Sequence Sequence Sequence

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US-08-446-692-20

| Sequence 20, Application US/08446692
| Sequence 20, Application US/08446692
| Sequence 20, Application US/08446692
| GENERAL INFORMATION:
| APPLICANT: Ladd, Anna | APPLICANT: Ladd, Anna | APPLICANT: Time of INVENTION: Immunogenic LHRH peptide constructs | TITLE OF INVENTION: Immunogenic LHRH peptide constructs | ITLE OF INVENTION: Internal immune stimulators for vaccines | NUMBER OF SEQUENCES: | As park Avenue | CITY: New York | COUNTY: US | CITY: New York | COUNTY: US | COUNTY: US | CITY: New York | CITY: New York | COUNTY: US | CITY: New York | CITY: New York | COUNTY: US | CITY: New York | CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 117; DB 1; Length 42; 82.8%; Pred. No. 4.7e-11; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUMTRY: US

ZIP: 10154-0053

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-005/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: T-UDN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 19.33

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acids
US-09-100-414B-38
US-09-303-323-38
US-09-770-014B-53
US-09-100-414B-53
US-09-70-014-53
US-09-70-014-53
US-09-303-323-60
US-09-303-323-60
US-09-100-414B-57
US-09-100-414B-57
US-09-100-414B-57
US-09-100-414B-57
US-09-100-414B-57
US-09-100-414B-50
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MOLECULE TYPE: peptide

US-08-446-692-20
          Query Match
Best Local Similarity
Matches 24; Conserv
          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 10, 2004, 08:58:54; Search time 12.0019 Seconds (without alignments) 133.345 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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Sequence
Sequence
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    /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-488-351A-19

US-08-488-351A-19

US-09-100-414B-19

US-09-700-14-36

US-08-446-692-33

US-08-446-692-33

US-09-700-14-43

US-09-700-014-43

US-09-700-014-43

US-09-700-014-43

US-09-700-014-43

US-09-700-014-43

US-09-700-014-43

US-09-700-014-44

US-09-700-014-41

US-09-700-014-41

US-09-700-014-41

US-09-700-014-41

US-09-700-014-41

US-09-700-014-41

US-09-700-014-45

US-09-700-014-41

US-09-700-014-41

US-09-700-014-45

US-09-700-014-41

US-09-700-014-41

US-09-700-014-45

US-09-700-014-41
                                                                                                                                                                                                                                                                                             US-09-848-834A-9
160
1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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Maximum DB
                                                                                                                                                OM protein
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Gaps

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GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Mang, Charby
THE APPLICANT: Anna
APPLICANT: Anna
APPLICANT: Anna
APPLICANT: Anna
APPLICANT: Anna
ANDERSON
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COUNTRY: US
COMPUTER INSTANCE
ZIP: NY
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: FAOPY disk
MEDIUM TYPE: FAOPY disk
MEDIUM TYPE: FAOPY disk
COMPUTER: PAOPY DISK
SOFTWARE: PATENT: PC-DCS/MS-DOS
SOFTWARE: PATENT: PC-DCS/MS-DOS
SOFTWARE: PATENT: PC-DCS/MS-DOS
SOFTWARE: PATENT: PC-DCS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION: C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
TELEPHONE: (312)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
72.5%; Score 116; DB 1,
Best Local Similarity 85.7%; Pred. No. 4e-11;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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Patent No. 5843446
        NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-488-351A-19
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                                                                                                                                                                                                                                                                                                                                                                                                  IRH peptide constructs universal immune stimulators for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.1%; Score 117; DB 2; Length 42; 82.8%; Pred. No. 4.7e-11; tive 1; Mismatches 2; Indels
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US-08-446-692-19
; Sequence 19, Application US/08446692
; Parent No. 5759551
; GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Mang, Thmothy
ITLE OF INVENTION: Immunogenic LHRH peptide constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ALLALLA.
CORRESPONDENCE ALLALLA.
ADDRESSEE: MATIG C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STRATE: NY
COUNTRY: US
ZIP: 10154-0633
COMPUTER: Floppy disk
COUNTRY: US
ZURPUTER: PREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPERATION SYSTEM: PC-005/MS-TOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1994
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1994
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION NUMBER: 1151-4146 US2
FILING DATE: 27-APR-1993
CLASSIFICATION NUMBER: 1151-4146 US2
FILING DATE: 27-APR-1993
CLASSIFICATION NUMBER: 1151-4146 US2
FILING DATE: 27-APR-1994
ATTORNEY/AGENT INFORMATION:
TELEPAK: (516)751-6449
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
FUNDORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
FUNDORMATION A A A MATHER A MATHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                               Sequence 20, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Ladd, Anna
APPLICANT: Mang, Chang Yi
APPLICANT: Mang, Chang Yi
TITLE OF INVENTION: Immunogenic LHRH
TITLE OF INVENTION: and synthetic un:
NUMBER OF SEQUENCES:
ADDRESSED: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.8
Matches 24; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-488-351A-20
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Gaps

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Indels
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Best Local Similarity 85.7%; Pred. No. 4e-11; Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 116;
Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LSEIKGVIVHRIEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
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Best Local Similarity 85.7%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                 RESULT 6
US-09-303-323-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGRATI INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REPRENDE/DOCKET NUMBER: 1151-4146 US2
TELECHONNICATION INFORMATION:
TELECHONE: (212)415-6849
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/09100414B
Setent No. 6025468
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
NAMES, CHANGEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES:
ADDRESSEE: ADDRESSE:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: NY
COMPUTER: NY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Word 97
CURRENT APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFFICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFFICATION: 424
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEC ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-100-414B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-09-100-414B-36
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Score 116;

72.5%;

Query Match

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Gaps
DB 3; Length 27;
                                             2; Indels
                                                                                                                                                                                                RESULT 7
US-09-770-014-36
Sequence 36, Application US/09770014
Sequence 36, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION
TILLE OF INVENTION: NOVEL LHRH PEPTIDE
TILLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
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STATE: N

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Sequence 33, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Mang, Chang Xi
APPLICANT: Wang, Chang Xi
APPLICANT: Wang, Chang Xi
APPLICANT: Wang, Chang Xi
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%; Score 116; DB 2; Length 45; 85.7%; Pred. No. 7.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
COMPUTER EACHLINE SELECT STATEM: PC-DCS/MS-DCS
SOFTWARE: TATEM: PC-DCS/MS-DCS
SOFTWARE: TATEM: PC-DCS/MS-DCS
SOFTWARE: TATEM: ACCOUNTINE SELECT STATEM: APPLICATION NUMBER: US/06/488,351A
FILING DATE: 7-UN-1995
CLASSIFICATION: A24
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRICK APPLICATION: A24
FILING DATE: 17-APR-1994
CLASSIFICATION: A24
FILING DATE: 27-APR-1994
CLASSIFICATION: A24
FRICK APPLICATION: A24
ATTORNEY/AGENT INFORMATION:
MAME: MATIA C.H. Lin
RECISEMATION NUMBER: 1151-4146 US2
TELECOMMONICATION NUMBER: 1151-4146 US2
TELECOMMONICATION NUMBER: 1151-4146 US2
TELECOMMONICATION NUMBER: 1151-4146 US2
                                                                                                                                                                                                              Query Match 72.5%; Score 116; DB 1; Best Local Similarity 85.7%; Pred. No. 7.3e-11; Matches 24; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                         3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                         19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44
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                       SEQUENCE CHARACTERISTICS:
| IENGTH: 45 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECULE TYPE: peptide
| US-08-446-692-33
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-488-351A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08446692
Sequence 33, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STREET: No York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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CZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 7.-UNN-1995
CLASSIFICATION: 424
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ATTORNEY TAKEN TO THE TO THE TAKEN TO THE TAKEN TO THE TAKEN TO THE TELECOMMUNICATION INPORMATION:

REFERENCE/DOCKET NUMBER: 1151-4146 US2
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212)415-8145
TELEFRAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BW PC compatible
CURRENT APPLICATION DATA:
FILING DATE: CLASSIFICATION:
FRICK APPLICATION NUMBER: US/09/770,014
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARIA H. Lin
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1151-4157
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-770-014-36
                       USA
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STATE: N
COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/09770014
Patent No. 655282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LIRH PEPTIDE
ITTLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPALIDLE
OPERATING SYSTEM: PC WINGOWS
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
                                                         SCHWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION DATA
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNBE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNB-1998
ATTORNEY/AGBNT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151-41:
TELECOMMUNICATION INFORMATION:
                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-751-6849
| INPORMATION FOR SEQ ID NO: 4;
| SEQUENCE CHARACTERISTICS:
| LENGTH: 27 amino acids
| TYPE: amino acids
| MOLECULE TYPE: peptide
| US-09-303-323-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-770-014-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
       Gaps
       5
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6228987
Patent No. 6228987
Patent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOSENS
TITLE OF INVENTION: IMMUNOSENS
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
    Mismatches
                                                                                                                                                                          GENUEL OF 100-414B-43

Sequence 43, Application US/09100414B

Sequence 43, Application US/09100414B

Patent No. 6025468

TELE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: INMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE MOTGAN & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSEIKGVIVHKLEGVGGE--HWSYGLRP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: New JOIN
COUNTRY: USA
ZIP: 10154-0054
ZIP: 10154-0054
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAAIA H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                        19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44
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Best Local Similarity 82.1*
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
       24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
// TYPE/LOGY: linear
// MOLECTLE TYPE: peptide
US-09-100-414B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-303-323-43
       Matches
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Score 110; DB 3; Length 31;
Pred. No. 4e-10;
1; Mismatches 5; Indels
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Sequence 55, Application US/09770014
Sequence 55, Application US/09770014
Sequence 55, Application US/09770014
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: 106
STREET: 345 Park Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LSEIKGVIVHKLEGVLFGGEHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                  SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 30-APR-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REPERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
            ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIF: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/ASCHY INCREMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                       COUNTRY: USA
ZIP: 10184-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , TOPOLOGY: linear
, MOLECULE TYPE: peptide
US-09-303-323-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-770-014-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
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                                                                                                                               Score 113; DB 4; Length 27; Pred. No. 1.2e-10; i Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-3013-25
Sequence 55, Application US/09303323
Sequence 55, Application US/09303323
Patent No. 6228987
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITX: New ACCURTATE NEW ACCURTATE NEW COUNTRY: USA

ZIP: 10154-0084

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATE: US/09/100,414B
FILING DATE: 20-UNE-1998
CILASSIFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTATION NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHRACATERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                             US-09-100-414B-55
; Sequence 55 Application US/09100414B
; Patenn No. 6025466
; Patenn No. 6025466
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: INMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LSEIKGVIVHKLEGVLFGGEHWSYGLRP 30
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                                                                                                                                                                                                                                                           1 LSEIKGVIVHKLEGVGGE--HWSYGLRP 26
                                                                                                                                    Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.6
Matches 22; Conservative
rrPB: amino acid
TOPOLOGY: linear
MOLECTULE TYPE: peptide
US-09-770-014-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps

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## REFERENCE/DOCKET NUMBER: 1151-4157
### TELECOMMUNICATION INFORMATION:
### TELEPAK: 212-758-4800
### TELEPAK: 212-758-4800
### TELEPAK: 212-758-6490
### TELEPAK: 212-751-6449
### INFORMATION FOR SEQ ID NO: 55:
### SEQUENCE CHARACTERISTICS:
### TOPOLOGY: 1 anino acid
### MOLECULE TYPE: peptide
### MOLECULE TYPE: pep
```

Sequence 12, Appl Sequence 11, Appl Sequence 20, Appl Sequence 20, Appl Sequence 30, Appl Sequence 30, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 31, Appl Sequence 41, Appl Sequence 41, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 34, Appl Sequence 34, Appl Sequence 32, Appl Sequence 32, Appl Sequence 33, Appl Sequence 34, Appl Sequence 32, Appl Sequence 33, Appl Sequence 34, Appl

us-09-848-834a-9.open.rapb

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FEATURE:
OTHER INFORMATION: Chimeric peptide made up of amino acid sequence 288-302 of the OTHER INFORMATION: asels virus fusion protein, F linked by a spacer peptide to aminother information: acid sequence 2-10 of the GnRH hormone
NAME/KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: Amidated Lysine
NAME/KEY: PEPTIDE
LOCATION: (1) ... (15)
OTHER INFORMATION: measles virus fusion protein, F
NAME/KEY: PEPTIDE
LOCATION: (19) ... (22)
OTHER INFORMATION: Spacer peptide
LOCATION: (23) ... (31)
OTHER INFORMATION: Peptide corresponds to amino acid sequences 2-10 of the human oTHER INFORMATION: Peptide corresponds to amino acid sequences 2-10 of the human oTHER INFORMATION: GNRH hormone
NAME/KEY: MOD_RES
LOCATION: (33) ... (31)
OTHER INFORMATION: GNRH hormone
NAME/KEY: MOD_RES
LOCATION: (31) ... (31)
    14 US-10-23-711-11

18 US-10-23-711-11

18 US-09-846-834A-19

19 US-09-747-802-30

10 US-09-747-802-30

10 US-09-747-802-30

10 US-09-865-294-8

10 US-09-865-294-8

10 US-09-865-294-8

10 US-09-865-294-8

10 US-09-87-233A-18

10 US-09-87-233A-20

10 US-09-87-233A-20

10 US-09-87-294-29

10 US-09-865-294-40

10 US-09-747-802-35

10 US-09-747-802-35

10 US-09-747-802-40

10 US-09-865-294-30

10 US-09-865-294-30

10 US-09-865-294-31

10 US-09-865-294-31
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09848834A;
Sequence 9, Application US/09848834A;
Patent No. US20020076416A1
GENERAL INPORMATION:
TILLE OF INVENTION: Chimeric Peptide Immunogens;
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: 04/09/848,834A;
CURRENT FILING DATE: 2001-05-04
FRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 200
SEQ ID NOS: 20
SEQ ID NO 9
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Aztificial Sequence
FEATURE:
RESULT 1
US-09-848-834A-9
  Sequence 17, Appli
Sequence 9, Appli
Sequence 33, Appli
Sequence 31, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 32, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Appli-
                                                                             March 10, 2004, 09:16:59; Search time 24.3658 Seconds (without alignments) 268.645 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-848-834A-9
US-09-848-834A-17
US-10-76-674-9
US-10-355-161A-9
US-09-847-102A-33
4 US-10-285-976-231
US-09-848-834A-13
US-09-848-834A-16
US-09-848-834A-16
US-09-848-834A-19
US-09-848-834A-8
US-10-285-976-229
US-09-848-834A-8
US-10-848-834A-8
US-10-848-834A-8
US-10-848-834A-1
                                                                                                                           US-09-848-834A-9
160.
1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX 31
                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                        809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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17585544005558
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Match Length
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                                                                                                                             Title:
Perfect score:
                                                                                                                                                                      Scoring table:
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Maximum DB 8
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                                                                                                                                                  Sequence:
                                                                                                                                                                                                        Searched:
                                                                                  Run on:
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No.
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US-09-847-102A-33

US-09-847-102A-33

Sequence 33, Application US/09847102A

Publication No. US20330044409A1

GENERAL INFORMATION:

APPLICANT: Carson, Dennis A.

APPLICANT: Carson, Dennis A.

APPLICANT: Corr, Maripat

APPLICANT: Rhee, Chae-Seo

APPLICANT: Rhee, Chae-Seo

APPLICANT: Malini, Seo

TITLE OF INVENTION: INMUNOLOGIC COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

TITLE OF INVENTION: DATE: 2001-05-01

CURRENT APPLICATION NUMBER: US/09/847,102A

CURRENT PILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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| Sequence 9, Application US/10355161A
| Publication No. US20040009897A1
| GENERAL INPORMATION:
| APPLICANT: Sokoll, Kenneth K.
| TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
| TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
| TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
| CURRENT APPLICATION NUMBER: US/10/355,161A
| CURRENT FILING DATE: 2003-01-31
| PRIOR PELLING DATE: 2002-02-14
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 9
| LENGTH: 45
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System FILE REFERENCE: Immunogen Delivery System CURRENT PEPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
72.5%; Score 116; DB 14;
Best Local Similarity 85.7%; Pred. No. 1.5e-09;
Matches 24; Conservative 0; Mismatches 2;
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-10-076-674-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human
US-10-355-161A-9
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ORGANISM: Affilicial Sequence
FEBTURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the GR
OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid sequence 288-302 of
OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid sequence 288-302 of
OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid sequence 1.10 of the GRH hormone
NAME/KEY: MOD_RES
LOCATION: (4.7)...(4.7)
OTHER INFORMATION: Amidated-glycine or glycinamide
NAME/KEY: PREPTIDE
LOCATION: (1)...(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GRH hormone
NAME/KEY: PEPTIDE
LOCATION: (1)...(18)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (29)...(34)
OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein,
NAME/KEY: PEPTIDE
LOCATION: (35)...(34)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (39)...(34)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GRH hormone
NAME/KEY: PEPTIDE
LOCATION: (39)...(47)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GRH hormone
NAME/KEY: PEPTIDE
LOCATION: (39)...(47)
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99.4%; Score 159; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                             Length 31;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09848834A

Sequence 17, Application US/09848834A

Patent NO. US20020076416A1

GENERAL INFORMATION:
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT APPLICATION NUMBER: 60/202,328

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR APPLICATION NUMBER: 60/202,328

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PRIOR TILING DATE: CONTINUED SOFTWARE: ATENTIAL 4.7

TYPE: PRI
SEQUENCE: CONTINUED SOFTWARE: PRIOR 
                 ; OTHER INFORMATION: Amidated glycine or glycinamide US-09-848-834A-9
                                                                                                                                    Ouery Match 99.4%; Score 159; DB 9; L. Best Local Similarity 100.0%; Pred. No. 5.8e-16; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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                                                                                                                                                                                                                                                                                                                                                                           1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                       1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-076-674-9
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OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of OTHER INFORMATION: he Measles virus fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRACTURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 947-967 of 10 OTHER INFORMATION: Tetanus toxoid precursor (Tentoxylysin) linked by a spacer to 60 OTHER INFORMATION: ino acid sequence 2-10 of the GnRH hormone NAME/KEY: MOD RES LOCATION: (1)...(1)
OTHER INFORMATION: Amidated phenylalanine OTHER INFORMATION: Amidated phenylalanine LOCATION: (1)...(21)
OTHER INFORMATION: Amino acids 947-967 of the Tetanus Toxoid Precursor OTHER INFORMATION: (Tentoxylysin)
NAME/KEY: PEPTIDE LOCATION: (25)
OTHER INFORMATION: Spacer peptide
                                                                                               MAMENCEY: PEPTIDE
LOCATION: (1)...(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnEH hormone
NAMENCEY: PEPTIDE
LOCATION: (11)...(18)
OTHER INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
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                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
LOCATION: (26)..(34)
OTHER INPOMATION: Amino acids 2-10 of the human GnRH hormone
NAME/KEY: MOD RES
LOCATION: (34)..(34)
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49.4%; Score 79; DB 9; Length 34;
Best Local Similarity 92.9%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 0; Indels
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, OTHER INFORMATION: Amidated glycine or glycinamide US-09-848-834A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-848-834A-10
| US-09-848-834A-10
| Sequence 10, Application US/09848834A
| Sequence 10, Application US/09848834A
| Sequence 10, US2000076416A1
| GENERAL INFORMATION |
| APPLICANT: Aphlon Corporation |
| TILE OF INVENTION: Chimeric Peptide Immunogens |
| FILE REPRENCE: 1102865-0047 |
| CURRENT APPLICATION NUMBER: US/09/848,834A |
| PRIOR APPLICATION NUMBER: 60/202,328 |
| PRIOR APPLICATION NUMBER: 60/202,328 |
| NUMBER OF SEQ ID NOS: 20 |
| SEQ ID NO 10 |
| SEQ ID NO 10 |
| LENGTH: 34 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.8%; Score 86; DB 9; Le
100.0%; Pred. No. 2.5e-05;
iive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
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SQUENCE 231, Application US/10285976

SQUENCE 231, Application US/0330165500A1

GENERAL INFORMATION:

SAPPLICANT: Rhed, Chae-Seo

APPLICANT: Malini, Sen

APPLICANT: Gerin, Lorenzo M.

APPLICANT: Corr, Maripat

APPLICANT: OF INVENTION: Who and Frizzled Receptors as Targets for Immunotherapy

TITLE OF INVENTION: Who and Frizzled Receptors as Targets

TITLE OF INVENTION: Who are an invention of the correct of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.9%; Score 99; DB 14; Length 75; Best Local Similarity 95.5%; Pred. No. 7.7e-07; Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                      Query Match 61.9%; Score 99; DB 10; Length 75; Best Local Similarity 95.5%; Pred. No. 7.7e-07; Matches 21; Conservative 0; Mismatches 1; Indels
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Patent No. US20020076416A1

GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REPERENCE: 1102865-004

FURBENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 05/02/328

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Version 3.0

LENGTH: 34

LENGTH: 34
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           OTHER INFORMATION: PMMVF-FZD2
                      ) OTHER INFORMA
US-09-847-102A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-285-976-231
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LENGTH: 75
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APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Carson, Dennis A.
APPLICANT: Carson, Dennis A.
APPLICANT: Carson, Leoni M.
APPLICANT: Rese, Chae-Seo
APPLICANT: Lorenzo, Leoni M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: INMUNOLOGIC COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FALLING DATE: 2001-05-01
SEQ ID NO 31
LENGTH: 75
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APPLICANT: Rain, Sen
APPLICANT: Malini, Sen
APPLICANT: Walini, Sen
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Corr, Maripat
APPLICANT: Cresson, Dennis A.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: In Head and Frizaled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT PILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
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                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                           Score 78; DB 14;
Pred. No. 0.00042;
0; Mismatches 1.
                                                                                                                                                                                                                  ) OTHER INFORMATION: synthetic construct US-10-223-711-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 229, Application US/10285976 Publication No. US20030165500A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-847-102A-31
Sequence 31, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KLLSLIKGVIVHRLEGVE 40
PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 40
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US-09-847-102A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-285-976-229
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CONTENT INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KENT: PREFINE
NAME/KENT: PREFINE
NAME/KENT: PREFINE
COCHIEN INFORMATION: Spacer peptide
NAME/KEY: PEPTION: (11)...(16)
NAME/KEY: PEPTION: (11)...(16)
NAME/KEY: PEPTION: (11)...(16)
OTHER INFORMATION: Oxylysin
NAME/KEY: PEPTION: (28)...(41)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTION: (28)...(41)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIOR
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIOR
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIOR
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human oTHER INFORMATION: GRRH linked by a spacer to amino acid sequence 947-967 of the Tet OTHER INFORMATION: anus toxoid precursor (Tentoxylyain) protein linked by a spacer to GTHER INFORMATION: o amino acid sequence 2-10 of human GRRH NAME/KEY: MOD_KES LOCATION: (1,1-,1)
OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD_KES LOCATION: (50)
OTHER INFORMATION: Amidated glycine or glycinamide
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Patent No. US20020076416A1
GENERAL INFORMATION:
APPLICANT: Aphton Ocrporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
TITLE REPRERNCE: 110265-004
FILLE REPRERNCE: 120365-004
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR PILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SEQTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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              20 LEGPSLHWSYGLRP 33
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OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 830-844 of 10 CTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 830-844 of 10 CTHER INFORMATION: Tetanus toxoid precursor (Tentcoxylysin) linked by a spacer to a OTHER INFORMATION: ino acid sequence 2-10 of the GnRH hormone NAME/KEY: MOD ESS LOCATION: (1)...(1)

OTHER INFORMATION: Amidated-glutamine NAME/KEY: MOD RES LOCATION: (28)

OTHER INFORMATION: Amidated-glycine or glycinamide OTHER INFORMATION: Amidated-glycine or glycinamide LOCATION: (28)

OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus Toxoid Precursor OTHER INFORMATION: (Tentcoxylysin)
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                                                                                                                                                                             Length 25;
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                                                                                                                                                                        Query Match

48.1%; Score 77; DB 15; 1
Best Local Similarity 72.0%; Pred. No. 0.00035;
Matches 18; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-848-834A-11
| Sequence 11, Application US/09848834A
| Patent No. US20020076416A1
| GENERAL INFORMATION
| TITLE OF INVENTION COIDERS.
| FILE REPRENCE: 1102865-0047
| CURRENT APPLICATION NUMBER: US/09/848,834A
| CURRENT PILING DATE: 2001-05-04
| PRIOR APPLICATION NUMBER: 60/202,328
| PRIOR APPLICATION NUMBER: 60/202,328
| PRIOR APPLICATION NUMBER: 60/202,328
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 11
| LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 73; DB 9; L
100.0%; Pred. No. 0.0015;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                            3 LSEIKGVIVHRLEGVEGPSLHWSYG 27
                                                                                                                                                                                                                                                                                                                         1 LSEIKGVIVHRLEGVGGFRHDSGYG 25
                                                                                                   ; OTHER INFORMATION: chimeric sequence US-10-411-544-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Spacer peptide NAMEKEY: PEPTIDE LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                 ORGANISM: Artificial sequence FEATURE:
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es 12; Conservative
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     LENGTH: 25
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Publication No. US20030232758A1
GENERAL INFORMATION:

Publication No. US20030232758A1
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: St. George-Hyslop, Peter
APPLICANT: McLaurin, Johane
TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzhe
TITLE OF INVENTION: Disease
FILE REPERENCE: L101547
CURRENT APPLICATION NUMBER: US/10/411,544
CURRENT FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
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                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 14; Length 75; Pred. No. 0.00085; O; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09848834A;
Patent No. US20020076416A1

GABREAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102665-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202,328
PRIOR PLING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION WIMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 229
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.4%; Pri
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLLSEIKGVIVHRLEGVE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KLLSLIKGVIVHRLEGVE 75
                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Measles virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: PEPTIDE
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US-10-411-544-32
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March 10, 2004, 08:58:54; Search time 9.64981 Seconds (without alignments) 309.015 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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160
1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX 31
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
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Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.	STIMMARIES
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	Description	fusion	l fusion	cell fusion glycop	F prot	cell fusion glycop	fusion	44	F prote	fusion	_	l fusion	l fusion	1 fusion	fusion	fusion	cell fusion protei	gonadoliberin prec	gonadoliberin prec	gonadoliberin prec	gene F protein - r	gonadoliberin prec	spike glycoprotein		gonadoliberin - sh		phosphoribosylamin	probable tetR-fami	hypothetical prote	conserved hypothet
SUMMARIES	QI	PQ0376	PQ0388	JU0274	847300	E48556	VGNZMV	VGNZRK	S47305	S47034	VGNZRL	JQ2223	VGNZCD	821382	AGNZPD	A48346	855386	RHHUG	RHMSG	RHRTG	847299	178541	VGVNFR	RHPGG	RHSHG	151423	DCBSPK	137168	T23151	AH0063
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æ	Query	45.0	45.0	45.0	45.0	45.0	45.0	44.4	44.4	41.6	41.2	40.6	40.6	40.6	40.0	40.0	37.5	35.9	35.6	35.6	35.0	33.8	33.1	32.5	32.5	32.5	32.5	31.6	31.2	30.6
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	30.6	30.3	30.3	30.0	30.0	30.0	30.0	30.0	30.0	29.7	29.7	29.7	29.4	29.4	29.4	29.4
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	49	48.5	48.5	48	48	48	48	48	48	47.5	47.5	47.5	47	47	47	47
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 PRO1376 Call fusion glycoprotein - measles virus (strain TT) (fragment) Call fusion glycoprotein - measles virus (strain TT) (fragment) Call fusion glycoprotein - measles virus (strain TT) (fragment) Chacessian Padda, virus Chacessian Padda, virus A.THILE A measles virus isolate from a child with Kawasaki disease: sequence comparise A.THILE A measles virus isolate from a child with Kawasaki disease: sequence comparise A.THILE A measles virus isolate from a child with Kawasaki disease: sequence comparise A.THILE A measles virus isolate from a child with Kawasaki disease: sequence comparise A.THILE A measles virus isolate from a child with Kawasaki disease: sequence comparise A.THILE A measles virus isolate from the comparise A.THILE A measles virus meanware fusion Charter of Call fusion glycoprotein meanware fusion Charter of Call fusion glycoprotein meanles virus (strain Schwarz vaccine) (fragment) C.Speciasi measles virus meanware fusion 17-Apr-1993 #text_change 24-Nov-1999 C.Speciasi measles virus solate virus (strain Schwarz vaccine) (fragment) C.Speciasi measles virus solate virus (strain Schwarz vaccine) C.Speciasi virus solate virus (strain Schwarz vaccine) C.Speciasi virus solate virus (strain Schwarz vaccine) C.Speciasi virus solate virus (strain Schwarz vaccine) C.Superiamily: parainfluenca virus call fusion protein C.Superiamily: parainfluenca virus call fusion protein C.Superiamily: parainfluenca virus (strain Schwarz virus old) C.Superiamily: parainfluenca virus (
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A; Molecule type: mRNA
A; Residues: 1-533 cBUC>
A; Cross-references: GB:D00090; NID:g222061; PIDN:BAA00056.1; PID:g222062
A; Experimental source: strain Halle
R; Richardson, C.; Hull, D.; Greer, P.; Hasel, K.; Berkovich, A.; Englund, G.; Bellini,
Virology 155, 508-523, 1986
A; Fitle: The nucleotide sequence of the mRNA encoding the fusion protein of measles vir
A; Reference number: A94350; MUID:87071668; PMID:3788062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; MOLGCUIE type: mRNA
A; Residues: 4-553 < RLC>
A; Residues: 4-553 < RLC>
A; Cross-references: GB-M14915; NID:g331762; PIDN: AAA46423.1; PID:g331763
A; Experimental source: strain Edmonston
R; Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, B.J.; Dillon, M.J.; Weiss, R.A.
G. Gen. Virol. 73, 1581-1586, 1992
A; Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisc
A; Reference number: PQ0374; MUID:92300360; PMID:1607874
                       C;Species: meaales virus
C;Species: meaales virus
C;Species: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Date: 17-Feb-1994 #sequence_revision: Hashimoto, H.; Makino, S.
R;Mori, T.; Saeaki, K.; Hashimoto, H.; Makino, S.
Virus Genes 7, 67-81, 1993
Virus Genes 7, 67-81, 1993
A;Title: Molecular clioning and complete nucleotide sequence of genomic RNA of the AIK-C
A;Reference number: A48556; MUID:93227570; PMID:8470368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Title: Fusion glycoprotein of measles virus: nucleotide sequence of the gene and comp. A.Reference number: A92794; MUID:87224816; PMID:3585281
A,Accession: A26962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: meaales virus
C.Date: 31-Mar-1988 #sequence revision 31-Mar-1989 #text_change 16-Jun-2000
C;Accession: A26962; A25616; PQ0380; PQ0384
ASBuckland, R.; Gerald, C.; Barker, R.; Wild, T.F.
J. Gen. Virol. 68, 1695-1703, 1987
                                                                                                                                                                                                                                                                                                                    A;Molecule type: genomic RNA
A;Reaidues: 1-550 «MOR>
A;Cross-references: GB:S58435; NID:g299460; PIDN:AAB26145.1; PID:g299465
A;Note: Bequence extracted from NCBI backbone (NCBIN:129264, NCBIP:129272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
E;1-2-2-10main: signal sequence #status predicted <SIG>
F;1-2-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-550/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;113-128/Region: hydrophobic
F;495-514/Domain: transmembrane #status predicted <TMM>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predic
fusion glycoprotein precursor - measles virus (strain AIK-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.0%; Score 72; DB 1; Length 550; 100.0%; Pred. No. 0.033;
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C,Superfamily: parainfluenza virus cell fusion protein
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A; Residues: 272-553 <SCH2>
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A, Residues: 272-553 <SCH1>
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R;Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Abescription: The complete nuclectide sequence of the fusion protein gene of the vaccin
A;Accession: 847300
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R;Chamberlain, R.W.; Wamwayi, H.M.; Hockley, E.; Shaila, M.S.; Goatley, L.; Knowles, N.J. Gen. Virol. 74, 2775-2780, 1993
J. Gen. Virol. 74, 2775-2780, 1993
A;Title: Exidence for different lineages of rinderpest virus reflecting their geographic A;Reference number: PQ0865; MUID:94103786; PMID:8277286
                                                                                                                                                                                                                                                                                         R;Komase, K.; Haga, T.; Yoshikawa, Y.; Sato, T.A.; Yamanouchi, K.
Virus Genes 4, 173-181, 1990
A;Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defe
A;Reference number: JU0274; MJID:90385702; PMID:1698327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-534 <KOM>
A;Cross-references: EMBL:D10548; NID:g222256; PIDN:BAA01405.1; PID:g222257
A;Note: the authors translated the codon GTA for residue 459 as Gly and GGG for residue
C;Genetics:
                                                                                                                 all fusion glycoprotein precursor - subacute sclerosing panencephalitis virus (strain contains: fusion glycoprotein F2, species: subacute sclerosing panencephalitis virus, SSPEV pate: 31-bec-1993 #sequence_revision 31-bec-1993 #text_change 16-Jun-2000
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Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Superfamily: parainfluenza virus cell fusion protein
C,Keywords: glycoprotein; membrane fusion; transmembrane protein
C,Keywords: glycoprotein; membrane fusion; transmembrane protein
F;122/Domain: signal sequence #status predicted <SIG>
F;23-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-534/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;498-514/Domain: transmembrane #status predicted <TMN>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
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Pred. No. 0.032;
0; Mismatches 0; Indels
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Pred. No. 0.033;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LSEIKGVIVHRLEGV 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LSEIKGVIVHRLEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-546 <EVA>
                                                                                                                                                                                                                                                                                 Accession: JU0274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
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Gaps

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284 LSEIKGVIIHRLEGV 298

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cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of th
                                                                                                                                                                                   C)Species: porpoise morbillivirus
C)Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C,Accession: 837034 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C,Accession: 837034 #sequence No. 1994 #s. Wishaupt, R.G.A.; Welsh, M.J.;
Submitted to the EMBL Data Library, July 1994
A,Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbil
A,Reference number: 847034
                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: 847034
A,Molecule type: mENA
A,Molecule type: mENA
A,Residues: 1-52 - ReDL.
A,Cross-references: EMBL:X80757; NID:G520639; PIDN:CAA56731.1; PID:g520640
A,Experimental source: isolate Ulster 88
A,Note: the source is designated as Cetacean morbillivirus
C;Superfamily: parainfluenza virus cell fusion protein
F;1-25,Domain: signal sequence #status predicted <SIG>
F;26-552/Product: fusion protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (covalent) #status predicted
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C, Keywords: glycoprotein; membrane fusion; transmembrane protein
E;1-1-19/Dománi: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F2 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66, DB 1, Length 546, Pred. No. 0.23; 0; Mismatches 1; Indels
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C;Species: phocine distemper virus
                                                                                                                        cell fusion protein precursor - porpoise morbillivirus N,Alternate names: F protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 LSEVKGVIVHRLEAV-----SYNL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LSEIKGVIVHRLEGVEGPSLHWSYGL 28
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 LSEIKGVIVHRLESV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LSEIKGVIVHRLEGV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 61.5 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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VGNZRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
JQ2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
NyContains: fusion glycoprotein F1; fusion glycoprotein F2
CiSpecies: rinderpest virus
CiSpecies: rinderpest virus
CiSpecies: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
CiAccession: A31051
RiHsu, D.; Yamanaka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A;Hitle: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis was A;Reference number: A31051, MUID:88322864; PMID:3413983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene F protein - rinderpest virus
Gispecies: rinderpest virus
Cispecies: rinderpest virus
Cispecies: rinderpest virus
Cispecies: rinderpest virus
Cispecies: 20-oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
Cispecies: 20-oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
Cispecies: 247305 #text.
Cispecies: M.D.; Barrett, T.
Ribaron, M.D.; Barrett, T.
Ribaron, M.D.; Barrett, T.
Alpescription: The sequence of the N and L genes of Rinderpest virus, and the 50 and 30
Alcoestation: 847305
Alcoestation: 847305
Alcoestation: 847305
Alcoestation: 847305
Alcoestation: Salvania virus
Cispecianily: parainfluenza virus cell fusion protein
Cikeywords: transmembrane protein
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A,Residues: 1-546 48U>
C,Genetics:
C,Genetics:
C,Superfamily: parainfluenza virus cell fusion protein
C,Keywords: glycoprotein, membrane fusion; transmembrane protein
C,Keywords: glycoprotein, membrane fusion; transmembrane protein
C,Keywords: glycoprotein, membrane fusion F2 #status predicted <FFI>F):10-546/Product: cell fusion glycoprotein F2 #status predicted <FFI>F):109-546/Product: cell fusion glycoprotein F1 #status predicted <FFI>F):109-134/Domain: transmembrane #status predicted <TNI>F):109-134/Domain: transmembrane #status predicted <TNI>F):10-515/ByBinding site: carbohydrate (Asn) (covalent) #status predicted
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F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-110/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:111-253/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:1511/Domain: transmembrane #status predicted <TMN>
F:501-517/Domain: transmembrane #status predicted <TMN>
F:32,64,70/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                             Score 72; DB 1; Length 553;
Pred. No. 0.033;
0; Mismatches 0; Indels
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Pred. No. 0.046;
1; Mismatches 0; Indels
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Pred. No. 0.046;
.; Mismatches
                                                                                                                                                                                                                            ilarity 100.0%; P. Conservative 0;
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93.3%;
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93.38;
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Best Local Similarity
Matches 14; Conserv
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Matches 15; Conserv
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cell fusion glycoprotein precursor - phocine distemper virus
N;Contains: fusion protein F1; fusion protein F2
C;Species: phocine distemper virus
C;Species: phocine distemper virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 25-Oct-1996
C;Accession: 00:368
R;Koevamees, J.; Blixenkrone-Moeller, M.; Sharma, B.; Oervell, C.; Norrby, E.
A;Gen: Virol. 72, 259-2966, 1991
A;Title: The nucleotide sequence and deduced amino acid composition of the haemagglutin A;Reference number: 00:368; MUID:92113538; PMID:1765768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Accession: A48346
R.Curran, M.D.; Lu, Y.J.; Rima, B.K.
Arch. Virol. 126, 159-169, 1992
A.Title: The fusion protein gene of phocine distemper virus: nucleotide and deduced ami
A.Reference number: A48346; MUD:92398437; PMID:1524494
A.Rocession: A48346
                   R;Wild, T.F.; Bernard, A.; Spenner, D.; Villeval, D.; Drillien, R.
submitted to the EMBL Data Library, April 1992
A;Description: Vaccination of mice against canine distemper virus induced encephalitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell fusion glycoprotein precursor - phocine distemper virus (strain Ulster/88) N;Contains: fusion protein F1; fusion protein F2 C;Species: phocine distemper virus C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 25-Oct-1996
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A,Residues: 1-631 <CUR>
A,Rote: sequence extracted from NCBI backbone (NCBIN:113098, NCBIP:113099)
C,Genetics:
A,Gene: F
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                                                                                                                                                                                                                                                                                                 A;cross_references: EMBL;X65509; NID:958853; PIDN:CAA46481.1; PID:958854 C;Superfamily: parainfluenza virus cell fusion protein
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C,Keywords: glycoprotein; membrane fusion; transmembrane protein
C,Keywords: glycoprotein F2 #status predicted <FP2>
F;1-188 Fyroduct: cell fusion glycoprotein F2 #status predicted <FP2>
F;189-105/Domain: transmembrane #status predicted <TM1>
F;189-103/Region: cleavage processing #status predicted
F;194-631/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;194-21/Domain: transmembrane #status predicted <TM2>
F;575-595/Domain: transmembrane #status predicted <TM3>
F;110,142,148,486/Binding site: carbohydrate (Asn) (covalent) #status F
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0.4;
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80.0%; Pred. No. 0.52;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                   40.6%; Score ilarity 86.7%; Pred. Conservative 1; Mis
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A, Residues: 1-631 <KOV>
                                                                                                                                                                                                             A, Status: preliminary
A, Molecule type: genomic RNA
A, Residues: 1-662 <WIL>
                                                                                                                                     A; Reference number: S21382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 13; Conser
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C;Accession: JS0321
R;Barrett, T.; Clarke, D.K.; Evans, S.A.; Rima, B.K.
Virus Res. 8, 373-386, 1987
A;Title: The nuclectide sequence of the gene encoding the F protein of canine distemper
A;Reference number: JS0321; MUID:88129050; PMID:3433924
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C) Superfamily: parainfluenza virus cell fusion protein
C) Superfamily: parainfluenza virus cell fusion; transmembrane protein
K-Rywordsen; glycoprotein: signal sequence #status predicted <SIGO.
F) 1-135/Domain: signal sequence glycoprotein F2 #status predicted <F2P>
F) 156-224/Product: cell fusion glycoprotein F1 #status predicted <F1P>
F) 506-629/Domain: transmembrane #status predicted <MEN.
F) 606-629/Domain: transmembrane #status predicted <MEN.
F) 61-11,173,179,517/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                            A, Accession: J02223
A, Molecule type: mRNA
A, Accession: J02223
A, Molecule type: mRNA
A, Cross-references: GB: L07075
A, Genetics: A, G
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cell fusion protein - canine distemper virus
C;Species: canine distemper virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell fusion glycoprotein precursor - canine distemper virus N;Contains: fusion protein F2
C;Species: canine distemper virus
C;Species: canine distemper virus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
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A;Residues: 1-662 <BAR>
A;Cross-references: GB:M21849; NID:g323241; PIDN:AAA42878.1; PID:g323242
C;Genetics:
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40.6%; Score 65; DB 2;
Best Local Similarity 86.7%; Pred. No. 0.32;
Matches 13; Conservative 1; Mismatches
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C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-188/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F;89-106/Domain: transmembrane #status predicted <TM1>
F;194-631/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;194-219/Domain: transmembrane #status predicted <TM2>
F;575-595/Domain: transmembrane #status predicted <TM3>
F;515-595/Domain: transmembrane #status predicted <TM3>
F;110,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Search completed: March 10, 2004, 09:16:45 Job time: 10.7086 secs

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EMBL; D10548; BAA01405.1; -.
HSSP; P04849; 1SVF.
InterPro; IPR000776; Fusion_gly.
Pfam, PF00523; fusion_gly; 1.
Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SIGNAL
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EXTRACELLULAR (POTENTIAL).
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LINKAGE BETWREN F2 & F1 (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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W-FSB21757E643844D CRC64;
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284.724 Million cell updates/sec
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                                                                              March 10, 2004, 08:58:53; Search time 5.66926 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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160
1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX
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Listing first 45 summaries
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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--- SUBNITI: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
--- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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-i- FUNCTION: This protein directs fusion of viral and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P26033;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
                                                                                                                           OBYDWS
P81615
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Viruses, ssRNA negative-strand viruses, Mononegavirales,
Paramyxoviridae, Paramyxovirinae, Morbillivirus.
VCBI_TaxID=11239;
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DFA2_ANASP
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VGLF_PITHC
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                                                                                                                                P35973;
                                                  RESULT 3
VGLF MEASA
ID VGLF M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; S47300; S47300.

HSSP, P04849; 1SVF.

INCERPIC; IPRO00776; Fusion_gly.

Pfam; PF00523; fusion_gly; I.

Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.

SIGNAL 1 19
                                                        Gaps
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--- SUBINIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
--- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUSION GLYCOPROTEIN FO.

P1 PROTEIN.
P1 PROTEIN.
ARG/LYS-RICH (BASIC).
POTENTIAL.
ARG/LYS-RICH (BASIC).
LINKAGE BETWEEN F2 & F1 (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.

BUBLINES-85088609, bubMed=7996154;

BVans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.,

"Nucleotide sequence comparisons of the fusion protein gene from
"Nucleotide sequence crafts of rinderpest virus.";

J. Gen. Virol. 75:361-3617(1994).

-: FUNCTION: This protein directs fusion of viral and cellular
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                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein precursor [Contains: Fusion glycoprotein Flusion glycoprotein glycoprotein gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 1; Length 546;
Pred. No. 0.0062;
0; Mismatches 0; Indels
DB 1; Length 534;
0.006;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rinderpest virus (strain RBT1) (RDV).
Viruses, ssRNA negative-strand viruses, Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38B539B89344F401 CRC64;
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                                                                                                                                                                                                                                                                                                             546 AA
Query Match 45.0%; Score 72; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 15; Conservative 0; Mismatches
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Local Similarity 100.0%; Pies 15; Conservative 0;
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                                                                                                                                            288 LSEIKGVIVHRLEGV 302
                                                                                                                 3 LSEIKGVIVHRLEGV 17
                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                       RESULT 2
VGLF_RINDB
ID VGLF_RIN
AC P41360;
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InterPro; IPR000776; Fusion_gly.
Pfan; PF00523; fusion_gly; I.
Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SIGNAL
CHAIN
24 550 FUSION GLYCOPROTEIN F0.
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-i-SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of genomic RNA
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
AAC4DAB92DE0D938 CRC64;
                                               01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion alycoprotein precursor (Contains: Rusion glycoprotein F2;
Fusion glycoprotein F1).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILIPE-93227570; PubMed=8470368;
MEDILIPE-93227570; PubMed=8470368;
Mori T., Sasaki K., Hashimoto H., Makino S.;
Molecular cloning and complete nucleotide sequence of genomic R the AIK-C strain of attenuated measles virus.";
Virus Genes 7.67-81(1993).
-:- FUNCTION: This protein directs fusion of viral and cellular
                                                                                                                                                                                                      Measles virus (strain AIK-C) (Subacute sclerose panencephalitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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PROTEIN F1.
POTENTIAL.
EXTRACELUTAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                    virus).
yiruse; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
yCgI_TaxID=36408;
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550 AA.
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PRT;
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nes 15; Conservative
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  STANDARD;
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P08300;
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VGLF MEASE
ID VGLF MI
AC P08300
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Gaps

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LSEIKGVIVHRLEGV 17

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Best Loc Matches

SEQUENCE FROM N.A.
STRAIN=Edmonston B;
Billeter N.A.,
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: This protein directs fusion of viral and cellular

Virology 202:665-672(1994) [7]

STRAIN=Edmonston;
MEDLINE=20085790; PubMed=2596022;
Cattance R., Schmid A., Spielhofer P., Kaelin K., Baczko K.,
Cattance R., Schmid A., Spielhofer P., Kaelin K., Udem S.A.;
Meulen V., Pardowitz J., Flanagan S., Rima B.K., Udem S.A.;
Mutated and hypermutated genes of persistent measles viruses which
caused lethal human brain diseases."; SEQUENCE FROM N.A.
STRAIN=Edmonston;
STRAIN=Edmonston;
SIRAIN=Edmonston;
Schmid A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V.,
Billeter M.A.;
Billeter M.A.;
altrations in the fusion protein cytoplasmic domain of the persisting measles virus.";
Virology 188:910-915(1992). SEQUENCE FROM N.A.
STRAIN-Edmonston;
MEDLINE=87071668; PubMed=3788062;
Richardson C.D., Hull D., Greer P., Hasel K., Berkovich A.,
Englund G., Bellini W.J., Rima B., Lazzarini R.A.,
"The nuclectide sequence of the mRNA encoding the fusion protein or massles virus (Edmonston strain): a comparison of fusion proteins from several different paramyxoviruses."; SECURNCE FROM N.A.
STRAIN-Halle,
MEDLINE-87224816; PubMed=3585281;
Buckland R., Gerald C., Barker R., Wild T.F.;
Brusion glycoprotein of measles virus: nucleotide sequence of the gene and comparison with other paramyxoviruses."; [3] SEQUENCE FROM N.A.

SEQUENCE FROM N.A.
STRAIN=Philadelphia-26;
MEDLINE=94303181; PubMed=8030232;
Hummel K.B., Vanchiere J.A., Bellini W.J.;
"Restriction of fusion protein mRNA as a mechanism of measles virus persistence."; SEQUENCE FROM N.A.
STRAIN=Edmonston, Leningrad-16, and Edmonston-Zagreb;
MEDLINE=94249203; PubMed=8191786;
Rota J.S., Wang Z.D., Rota P.A., Bellini W.J.;
"Comparison of Sequences of the H, P, and N coding genes of measles virus vaccine strains.";
Virus Res. 31:317-330(1994).

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-!- SUBNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family. PROTEIN FI.
PROTEIN FI.
PROTEIN FI.
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
LINKAGE BETWEEN F2 & F1 (POTENTIAL).
N-LINKED (GLONAC...) (POTENTIAL).
N-LINKED (GLONAC...) (POTENTIAL).
N-LINKED (GLONAC...) (POTENTIAL).
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EMBL; NOS97; CAA29090.1; ALT_INIT.

DR EMBL; KO1711; AAA7498.1; ALT_INIT.

DR EMBL; KO1711; AAA7498.1; ALT_INIT.

DR EMBL; U03659; AAA5660.1; ALT_INIT.

DR EMBL; U03659; AAA5660.1; ALT_INIT.

DR EMBL; U03659; AAA5660.1; ALT_INIT.

DR EMBL; U03670; AAA5660.1; ALT_INIT.

DR EMBL; CAA91360.1; ALT_INIT.

NA Glycoprotein; Fusion protein; Fu Length 550; Score 72; DB 1; Length 550 Pred. No. 0.0062; 0; Mismatches 0; Indels 45.0%; Sco. 100.0%; Pred 0; M 67 N-59532 MW; 3 LSEIKGVIVHRLEGV 17 Conservative Query Match Best Local Similarity 24 113 113 113 113 137 495 616 61 59 61 50 AA; DOMAIN DISULFID CARBOHYD CARBOHYD CARBOHYD SEQUENCE 288 STATE TETT TETT TO BE SEEN TO SEE THE 셤

RESULT 5
VGLF RINDR

AC P41356,
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2000 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F1.
DE Rusion glycoprotein F1.
CN Rinderpest virus (strain RBOK) (RDV).
CC Viruses; SRRNA negative-strand viruses; Mononegavirales;
CC Viruses; SRRNA negative-strand viruses.
CC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
CX NCBI TaxID=36409;
RN [1]

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                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP, PO4849; ISVP.
INTERPRO; PR000776; Pusion gly.
Pfam; PP00523; fusion gly; I.
Pfam; PP00523; fusion protein; Transmembrane; Envelope protein; Signal.
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Hsu D., Yamanaka M., Miller J., Dale B., Grubman M., Yilma T.;

Hsu D., Yamanaka M., Miller J., Dale B., Grubman M., Yilma T.;

"Cloning of the fusion gene of rinderpest virus: comparative sequence

analysis with other morbilliviruses.";

Virology 166:149-153(1988).

-i- FUNCTION: This protein directs fusion of viral and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULPIDE BOND.
-i- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
                                                               membranes.
--- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
---- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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F1 PROTEIN.
F2 PROTEIN.
F2 PROTEIN.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N-LINKAGE BETWEEN F2 & F1 (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
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01-0cT-1989 (Rel. 12, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein Precursor [Contains: Fusion glycoprotein F2,
FUNCTION: This protein directs fusion of viral and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 1; Length 546;
Pred. No. 0.048;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rinderpest virus (strain Kabete O) (RDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
VCBI_TaxID=11242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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58911 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M20870; AAA47399.1; -.
PIR; A28921; VGNZRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 LSEIKGVIVHRLESV 298
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SEQUENCE FROM N.A.
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AC P12574;
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DT 10-0CT-2;
DE Fusion g;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL, Z30697; CAA83181.1; -.
PIR, S47305, S47305.
InterPro; IPR000776; Fusion gly.
Pfam; PF00523; fusion gly.
Sqlycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SIGNAL
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-- SUBUNI: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOWN.
--- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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FI PROTEIN.
ARG/LYS-RICH (BASIC).
POTENTIAL.
POTENTIAL.
POTENTIAL.
ARG/LYS-RICH (BASIC).
LINKAGE BETWEEN F2 & F1 (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
W. EDJDF8AFFDBECR95 CRC64;
                                                     MEDIINE-95088609; PubMed=7996154;
Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
"Nucleotide sequence comparisons of the fusion protein gene from
virulent and attenuated strains of rinderpest virus.";
J. Gen. Virol. 75:361-3617(1994).
-!- FUNCTION: This protein directs fusion of viral and cellular
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16-OCT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein Precursor [Contains: Pusion glycoprotein F2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88219541; PubMed=3285575;
Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
"Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the F mXNA, and several features of the F protein."; Virology 164:523-530(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rinderpest virus (strain L) (RDV).
Viruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11243;
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VGLF_RINDL
ID VGLF_RINDL
AC P10864;
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CARBOHYD CARBOHYD SEQUENCE

Query Match

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                  EMBL; M21514; AAA47400.1; -.
PIR; A31051; 'VGNZKK.
INCEPPO; 18449; 1SVF.
INCEPPO; IPR000776; Fusion gly.
Pfam; PF00523; fusion gly/; 1.
Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SIGNAL
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SEQUENCE FROM N.A.
BARDILNE=88129050; PubMed=3433924;
BARDILNE=88129050; PubMed=3433924;
BARDILNE=88129050; PubMed=3433924;
The nucleotide sequence of the gene encoding the F protein of canine distemper virus: a comparison of the deduced amino acid sequence with Virus Res. 8:373-386(1987).
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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PROTEIN.

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N-LINKAGE BETWEEN F2 & F1 (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
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AC VGLF_CDVO STANDARD; PRT; 662 AA.

AC P12569; 065991;

DT 01-0CT-1989 (Rel. 12, Created)

DT 01-0CT-1989 (Rel. 12, Last sequence update)

DT 16-0CT-2001 (Rel. 40, Last annotation update)

DE Fusion glycoprotein F1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 93227696; PubMed=8470428; Wild TF., Bernard A., Spehner D., Villeval D., Drillien R.; Wild TF., Bernard A., Spehner D., Villeval D., Drillien R.; Wild Thirton of mice against canine distemper virus-induced encephalitis with vaccinia virus recombinants encoding measles canine distemper virus antigens."; Vaccine 11:438-444(1993).
-- FUNCTION: This protein directs fusion of viral and cellular
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                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 546; Pred. No. 0.068;
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1 Similarity 86.7%;
13; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M21849; AAA42878.1; --
EMBL; X65509; CAA46481.1; --
EMBL; X65509; CAA46481.1; --
EMBL; X65509; CAA46481.1; --
FIR, J6321; VGNZCD.
FIR, S21380; S21380.
HSSP; P04849; ISVF.
InterPro; IPR000776; Fusion gly.
InterPro; Fusion gly.
InterPro; IPR000776; Fusion gly.
INTERPRO* IPR000776; Fusion gly.
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VGLF MEASI

D VGLF MEASI

STANDARD; PRT; 529 AA.

10 VGLF MEASI

STANDARD; PRT; 529 AA.

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Fusion glycoprotein precursor (Contains: Fusion glycoprotein F2;

DE Fusion glycoprotein F1].

SW Measles virus (strain IP-3-Ca) (Subacute sclerose panencephalitis viruses; SSRNA negative-strand viruses; Mononegavirales;

OC Viruses; SSRNA negative-strand viruses; Mononegavirales;

OC Viruses; SSRNA negative-strand viruses; Mononegavirales;

NN NEDIT TAXID=11237;

RN MEDITURE-22563801; PubMed=1585658;

RN MEDITURE-22563801; PubMed=1585658;

RA SCHWIG FNOW N.A.

RA SCHWIG A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V., RA Billeter M.A.;

RY SEQUENCE FLOW INDEASING PROBLEM CONTROPARACTERIZED BY A LICERATIONS in the fusion protein cytoplasmic domain of the Viral measles virus.";

RY PETSISING measles virus.";

RY PETSISING measles virus.";

RY VIRIOGY 188:910-915(1992).

CC --- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 CC LINKED BY A DISULFIDE BOND.

CC --- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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--- SUBONT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
--- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

R -> K (IN REF. 2).

D -> N (IN REF. 2).

I -> M (IN REF. 2).

I -> M (IN REF. 2).

A -> V (IN REF. 2).

A -> V (IN REF. 2).

A -> H (IN REF. 2).
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Pred. No. 0.083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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P49921;
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Matches
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Cr send an emait.

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CR EMBL; X16566; CAA34567.1; -.

DR EMBL; X16566; CAA34569.1; ALT_INIT.

DR HSSP; Pod4849; 1SVF.

DR HSSP; Pod4849; 1SVF.

DR HSSP; Pod4849; 1SVF.

DR HSSP; Pod4849; 1SVF.

DR HSSP; Pod6849; 1SVF.

DR HSSP; Pod6849; 1SVF.

DR HSSP; Pod6849; 1SVF.

DR HSSP; Pod6849; 1SVF.

TANISMEM 116 529 PROTEIN F2.

FT CHAIN 127 1S PROTEIN F2.

FT CHAIN 116 529 PROTEIN F1.

FT TANISMEM 116 139 POTENTIAL.

TANISMEM 140 497 EXTRACELUTAR (POTENTIAL).

TANISMEM 140 497 EXTRACELUTAR (POTENTIAL).
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The nucleotide sequence and deduced amino acid composition of haemagglutinin and fusion proteins of the morbillivirus phocid
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STRAIN=1800late DK88-4A;
MEDLINE=92113538; PubMed=1765768;
Koevamees J., Blixenkrone-Moeller M., Sharma B., Oervell C..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%; Score 64; DB 1; Length 529; 93.3%; Pred. No. 0.093; ive 0; Mismatches 1; Indels
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE987BC9F07E9AA9 CRC64;
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J. Gen. Virol. 72:2959-2966(1991)
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Arch. Virol. 126:159-169(1992)
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Best Local Similarity 93.3%;
Marches 14; Conservative
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       SO THE PRESENTATION OF THE
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Pfam; PF00522; fusion gly; 1.
Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SIGNAL 1 1 CHAIN ? 631
MEDINE 19108508; PubMed=2264246; Curran M.D., Loan D.O., Rima B.K., Kennedy S.; Curran M.D., Loan D.O., Rima B.K., Kennedy S.; "Nucleotide sequence analysis of phocine distemper virus reveals its distinctness from canine distemper virus."; Vet. Rec. 127:430-431(1990).
                                                                                                                                                                                                       -!- SUBENIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
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F1 PROTEIN.
LINKAGE BETWEEN F2 & F1 (POTENTIAL).
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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1-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 1 Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
Fudeinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GRH I) (Luliberin I); GRH-associated peptide I]
GNRH1 OR GNRH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Weener G.D., Matteri R.L., Becker B.A.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V (IN REF. 2).
D1FC87CDD426E9B8 CRC64;
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LSEVKGVVVHRLEAV 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A48346; A48346.
PIR; JQ1368; VGNZPD.
HSSP; P04849; 1SVF.
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sapiens (Human)

us-09-848-834a-9.open.rsp

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nomo bapiens (numan).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                     Nature 311:666-668(1984).
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     hormone.
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                         releasing
                                                                                                                                              hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRATUM
                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the GnRH family.

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                                                                                                                                                                                                                                                        MEDLINE=72117544; PubMed=4946275;
Baba Y., Arimura A., Schally A.V.;
"On the tryptophan residue in porcine LH and FSH-releasing hormone.";
Blochem. Blophys. Res. Commun. 45:481-487 (1971).
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L32864; AAA31066.1; -.
InterPro; IPR002012; GnRH.
InterPro; IPR004079; GonadoliberinI.
Pfam; PF00446; GnRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSTIE; PS04773; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Placenta; Signal; Pyrrolidone carboxylic acid.
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                                                                                                                                                                             the solid-
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01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (Gonadotropin-releasing peptide I)
SEQUENCE OF 24-33.
MEDIANE-72114303; PubMed=4946067;
Baba Yu., Matsuo H., Schally A.V.;
"Structure of the porcine LH- and FSH-releasing hormone. II.
"Structure of the proposed structure by conventional sequential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-34 PROVIDE AMIDE GROUP) 8340474F32DDAA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57.5; DB 1; Length 91;
Pred. No. 0.14;
                                                                                                                             SYNTHESIS OF GONADOLIBERIN.
MEDLINE=72065376; PubMed=4942726;
Materio H., Arimura A., Nair R.M.G., Schally A.V.;
Mythesis of the porcine LH- and FSH-releasing hormone by phase method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE
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                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 45:822-827(1971).
                                                                                                Biochem. Biophys. Res. Commun. 44:459-463(1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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33 33
91 AA; 10090 MW;
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                                                                                                                                                                                                                                            SYNTHESIS OF GONADOLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
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P01148;
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SIGNAL
                                                                                    analyses.
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PEPTIDE
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peptide I]. GNRH1 OR GNRH OR LHRH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gonadotropins; it stimulates follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                   MEDIINE-66094338; PubMed=2867548;
Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
"Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat.";
                                                                                                         MEDIINE=89366682; PubMed=2671939;
Hayflick J.S., Adelman J.P., Seeburg P.H.;
"The complete nucleotide sequence of the human gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT SER-16.
MEDLINE-99318093; PubMed=10391209;
Cargill M., Aleshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Eriedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O., Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted.
PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
Lutrepulse or Lutrelef (Ferring Pharmaceuticals) and Relisorm
                                                                                                                                                                                                                                                                                                                                                                                                                Seeburg P.H., Adelman J.P.; "Characterization of cDNA for precursor of human luteinizing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
              Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 24-33.
MEDLINE-83126573; PubMed=6760865;
Tan L., Rousseau P.;
Tan Lie, Rousseau P.;
Lie chemical identity of the immunoreactive LHRH-like peptide biosynthesized in the human placenta.";
Eiochem. Biophys. Res. Commun. 109:1061-1071(1982).
                                                                                                                                                                                                                                                                                                                     factor in human and rat."; Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the GnRH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet, 23:373-373(1999).
-!- FUNCTION: Stimulates the secretion of the secretion of both luteinizing and
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANT SER-16.
MEDLINE=85012739; PubMed=6090951;
                                                                                                                                                                                    Nucleic Acids Res. 17:6403-6403 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human genes.";
Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X01059; CAA25526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M12578; AAA35916.1; -. EMBL; X15215; CAA33285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, S05308, RHHUG.
Genew, HGNC:4419, GNRH1.
MIM, 152760, -.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             90 AA;
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MOD_RES
SEQUENCE
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                                                                                                                                                                     CHAIN
PEPTIDE
PEPTIDE
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                                                                                                                                                        SIGNAL
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GON1 RAT
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R GO; GO:0005625; C:soluble fraction; TAS.

R GO; GO:0005183; F:luteinizing hormone-releasing factor activity; TAS.

R GO; GO:0007267; P:cell-cell signaling; TAS.

R GO; GO:0007275; P:negative regulation of cell proliferation; TAS.

R GO; GO:0007165; P:ingall transduction; TAS.

R INCEPPO: IPROMODIS: P:negative regulation of cell proliferation; TAS.

R INCEPPO: IPROMODIS: GRAH.

R INCEPPO: IPROMODIS: GRAH.

R PRINTS: PRO1441; GONADOLIBRNI.

R PROSTTE: PSO0445; GNRH: 1.

R PROSTTE: PSO04473; GNRH: 1.

R PLANGE ON pair of basic residues; Hormone; Amidation; Hypothalamus; M Placenta; Pharmaceutical; Signal; Polymorphism;

R Princildone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURNCE FROM N.A. MEDLINE=8706928; PubMed=3024317; MEDLINE=87069928; PubMed=3024317; Mason A.U., Hayfilick U.S., Zoeller R.T., Young W.S. III, Phillips H.S., Nikolics K., Seeburg P.H.; Phillips H.S., Nikolics K., Seeburg P.H.; Faletion truncating the gonadotropin-releasing hormone gene is responsible for hypogonadism in the hpg mouse."; Science 234:1366-1371(1986).
-:- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Prognandoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
[Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GRRH I) (Luliberin I); Prolactin release-inhibiting factor
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                    GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                 ACTIVITY.

PYRACLIDONE CARBOXYLIC ACID.

AMIDALION (G-34 PROVIDE AMIDE GROUP).

A -> S (in dbSNP:6185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                       Match 35.9%; Score 57.5; DB 1; Length 92; Local Similarity 80.0%; Pred. No. 0.14; es 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 013943.
30A72221B076FA79 CRC64;
                                                                                                                                                                                                                                     PROGONADOLIBERIN I.
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-!- SIMILARITY: Belongs to the GnRH family.
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                                                                                                                                                                                                                                                                                                                                                                                10380 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 VEG-PSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 VEGCSSOHWSYGLRP 32
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P13562;
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PEPTIDE
ACT_SITE
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GON1 MOUSE
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Matches
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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Prognandoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
[Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GRRH I) (Luliberin I); Prolactin release-inhibiting factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.; "Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotrophir-releasing hormone and prolactin release-inhibiting factor in human and rat." [
EMBL; M14872; AAA37717.1; -.
PIR; A47578; RHMSG.
MGD; MGI:95789; GDRh.
InterPro; IPR004079; GORA
InterPro; IPR004079; GonadoliberinI.
InterPro; PR004679; GRRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSTITE; PS06473; GRRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSTITE; PS06473; GRRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                  PROLACTIN RELEASE-INHIBITING FACTOR I. APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-32 PROVIDE AMIDE GROUP).
1C0766FA4826E4D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=8938461; PubMed=2476669;
Bond C.T., Hayflick J.S., Seeburg P.H., Adelman J.P.;
High rat gonadotropin-releasing hormone: SH locus: structure and
hypothalamic expression.";
Mol. Endocrinol. 3:1257-1262(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                          5
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MEDLINE=93105480; PubMed=1468115;
Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E.;
"Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone-releasing hormone mRNA.";
Cell. Mol. Neurobiol. 12:447-454 (1992).
                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1; Length 90;
Pred. No. 0.17;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Heart;
MEDLINE=87149087; PubMed=3547652;
Adelman J.P., Bond C.T., Douglass J., Herbert E.;
                                                                                                                                                                                                               PROGONADOLIBERIN I.
                                                                                                                                                                                                                                 GONADOLIBERIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=86094338; Pubmed=2867548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 LEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGCS--SQHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                       35.68;
                                                                                                                                                                                                                                                                                                                                                  10337 MW;
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nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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.. H us-09-848-834a-9.open.rsp

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"Developmental expression of the genes encoding transforming growth factor alpha and its receptor in the hypothalamus of female rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: March 10, 2004, 09:13:52
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ACT_SITE
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SEQUENCE
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-gib.ch/announce/or send an email to license@isb-sib.ch).
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                           Science 235:1514-1517(1987).
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROLACTIN RELEASE-INHIBITING FACTOR I. APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
    mammalian genes transcribed from opposite strands of the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (IH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 1; Length 92; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMII
494B5C64DA8A3EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROGONADOLIBERIN I.
                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Central nervous system.
-!- SIMILARITY: Belongs to the GRRH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GONADOLIBERIN
                                                                                                                                                                                                                                              EMBL; S50870; AAB24572.1; -.
EMBL; M12579; AAA41263.1; -.
EMBL; M31670; AAA41264.1; -.
EMBL; M15529; AAA42141.1; ALT_SEQ.
EMBL; M15529; AAA42139.1; -.
EMBL; M15528; -; NOT_ANNOTATED_CDS.
PIR; A40147; RHRTG.
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002012; GnRH.
InterPro; IPR004079; GonadoliberinI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hypothalamus;
MEDLINE=95124501; PubMed=7545971;
Ma Y.J., Costa M.E., Ojeda S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10500 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00446; GnRH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
GNRH1 OR GNRH OR LHRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA;
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PEPTIDE
ACT_SITE
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SEQUENCE
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GON1_MACMU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                        stimulates
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PIR, 178541; 178541.
InterPro; IPR002012; GRBH.
InterPro; IPR004079; GnadoliberinI.
PROM-PRO; PR00467; GRRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSTIE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal; Pyrrolidone carboxylic acid.
NON_TER 1
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AMIDATION (G-16 PROVIDE AMIDE GROUP) (BY
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APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY (BY SIMILARITY).
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                             Neuroendocrinology 60:345-3591934).
-- FUNCTION: Stimulates the secretion of gonadotropins; it st
the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID (BY
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Pred. No. 0.35;
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PROGONADOLIBERIN I.
GONADOLIBERIN I.
                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
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macaques. ";
Neuroendocrinology 60:346-359 (1994)
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7573 MW;
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MEDLINE=89003063; PubMed=3167982;
Cattaneo R., Schmid A.; Bschle D., Baczko K., ter Meulen V.,
Billeter M.A.;
"Bised hypermutation and other genetic changes in defective measles viruses in human brain infections.";
cell 55:255-265(1988).
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Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 15; Conservative 0; Mismatches 0; Indels
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Pfan; PPO:0523; Rialon gly; I. SEQUENCE 534 AA; 57899 MW; 637245E21B5BE044 CRC64;
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Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
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Cattaneo R., Billeter M.A.;
Virology 0:0-0(0).
EMBL; X16569; CAA34581.1; -.
EMBL; X16569; CAA34582.1; -.
HSSP; P04849; ISVF.
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Q04243,
01-NOV-1996 (TEMBLrel. 01,
01-NOV-1996 (TEMBLrel. 01,
01-JUN-2003 (TEMBLrel. 24,
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Fusion protein.
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319.245 Million cell updates/sec
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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160
1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX
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Maximum Match 100%
Listing first 45 summaries
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sp_unclassified:*
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"Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated predicted secondary structure changed.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF179440; AAF02705.1; --
EMBL; AF179439; AAF02706.1; --
HSSP; PO4649; LSVF.

GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Biased hypermutation and other genetic changes in defective measles viruses in human brain infections."; Cell 55:255-265(1988).
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Ogura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-80013063; Pubmed=3167982;
Cartaneo R., Schmid A., Eschle D., Baczko K., ter Meulen V.,
Billeter M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.0%; Score 72; DB 12; Length 537; 100.0%; Pred. No. 0.073; Live 0; Mismatches 0; Indels
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Q9PXA4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Fusion protein.
Measles virus.
Viruses; sexNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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                                                           537 AA
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                                                           PRT;
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Virology 0.0-0(0).
EMBL, X16567, CAA34574.1; --
EMBL, PO4849; 1SVP.
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MEDLINE=21014265; PubMed=11186456;
Alanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
Alanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
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45.0%; Score 72; DB 12; Length 546;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 15; Conservative 0; Mismatches 0; Indels
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EMBL; AV035887; AAK63190.1; -.

PIR; PQ0866; PQ0866.

PIR; PQ087; PQ0867.

GO; GO:0019039; P:viral-cell fusion molecule activity; IBA.

GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

InterPro; PR000776; Fusion gly.

Eam; PF00623; fusion gly.

SEQUENCE 546 AA; 58572 MW; 4492B2DD7405F0B CRC64;
                                                                                                                                                                                                                       Length 545;
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Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBI_TaxID=11234;
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GO; GO:0006948; P:viral-induced cell-cell fusion; IEA
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Last annotation update)
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100.0%; Pred. No. 0.074;
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                                                 InterPro; IPR000776; Fusion gly. Pfam; PF00523; fusion gly; 1. SEQUENCE 545 AA; 58907 MW; 0:
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100.0
Matches 15; Conservative
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AC P9033
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"Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or
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Pred. No. 0.075;
                          Score 72; DB 12; Length 550;
Pred. No. 0.075;
0; Mismatches 0; Indels
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Pfam; PF00523; fusion gly.
SEQUENCE 550 AA; 59405 WW; OAEGDBFC5DB2BBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
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STRAIN=Nagahata(HB);
Sheng J., Watanabe M., Ueda S.;
Sheng J., Watanabe M., Ueda S.;
Selection of a neurotropic variant of measles virus.";
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR179436; AAF02701.1; -...
PIR; PQ0376; PQ0376.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pre
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01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 11-0CT-2003 (TrEMBLrel. 25,
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                                                                                         Local Similarity
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"Nucleotide sequences of the fusion protein gene of subacute schorosing panemephalitis viruses."

"Nucleotide sequences of the fusion protein gene of subacute schorosing panemephalitis viruses."

"In showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";

"Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; D63956; BAA09958.1; --

"REBL; AF179431; AAF02696.1; --

"REBL; AF179431; AAF02696.1; --

"REBL; P004649; ISVP.

"REBL; P004649; ISVP.

"RO; GO:0010939; F:viral-cell fusion molecule activity; IEA.

"GO; GO:0010939; F:viral-cell fusion molecule activity; IEA.

"RO; GO:0010939; F:viral-cell fusion gly."

"RIFEPPRO; PRO00574; Fusion.gly."

"REPROSED: PF00623; fusion.gly."

"REPROSED: PF00623; fusion.gly."

"REPROSED: PF00623; fusion.gly."

"REPROSED: PF00623; fusion.gly."

"REPROSENCE 550 AA; 59530 MW; 97C991C7E2169839 CRC64;
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"Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF179432; AAF02697.1; --
PIR; PQ0376; PQ0376.
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Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBL_TaxID=11234;
                                                                                    SEQUENCE FROM N.A.
STRAIN=NAGAHATA;
Sheng J., Watanabe M., Ueda S.;
Sheng J., Watanabe M., Ueda S.;
Selection of a neurotropic variant of measles virus.";
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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eqn aa: 59504 MW; 2AA969D37FA5CA17 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NAGAHATA;
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SEQUENCE
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RESULT 6 090EX0

Matches

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Q8V049
ID Q8V04
AC Q8V04
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RI predicted secondary structure changed.";

RI Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

BR BL; PQ4319, AAF02703.1; -.

BR HSSP; PQ4849; ISVF.

GO; GO:0019939; F:viral-cell fusion molecule activity; IEA.

GO; GO:0019948; P:viral-induced cell-cell fusion; IEA.

BR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

BR HSP: PRO523; fusion gly: 1.
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STRAIN=OSA-2;
Ning X., Ayata M., Morimoto X., Ito N., Shingai M., Kimura M.
                                                                                                                                                                              Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 15; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 15; Conservative 0; Mismatches 0; Indels
fusogenicity of measles virus.";
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D63924; BAA09951.1; -.
PIR; P00376; P00376.
HSSP; P04849; ISYP.
GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
GO; GO:0019039; F:viral-induced cell-cell fusion; IEA.
InterPro; IPR000776; Pusion gly.
InterPro; IPR000776; Pusion gly.
Exaction FP00529; Etusion gly; I.
SEQUENCE 550 AA; 59589 MW; 73B7BD457ABA39B7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 25, Last annotation update)
Fusion procein.
Wasales virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBI_TaxID=11234;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q9QEW7
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MEDLINE=9329215; PubMed=10400788;

A Schneider-Schaulies J.,

Schneider-Schaulies J.,

A schneider-Schaulies J.,

The recombinant measle vaccine virus expressing wild-type

The glycoproteins: consequences for viral spread and cell tropism.";

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Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 45.0%; Score 72; DB 12; Length 550; Best Local Similarity 100.0%; Pred, No. 0.075; Matches 15; Conservative 0; Mismatches 0; Indels
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fusion protein.
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08V049;
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01-MAR-2002 (
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CENTAIN=Magusako;

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AND X.A. Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,

AND X.A. Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,

AND X.A. Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,

AND X.A. Ayata M., Morimoto K., Ito N., Shingai M.,

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NING X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
A Ogura H.; Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
Invaledtide sequences of the fusion protein gene of subacute
sclerosing panencephalitis viruses: deduced amino acid sequences
of sclerosing panencephalitis viruses: deduced amino acid sequences
of sclerosing panencephalitis viruses: deduced amino acid sequences
of predicted secondary structure changed.";
Spredicted secondary structure changed.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

BMBL, AF179437; AAF02702.1;
BMBL, AF179437; AAF02702.1;
CO. GO:0019035; F. Pizzal-cell fusion molecule activity; IEA.
CO. GO:0019039; F. Vizzal-cell fusion molecule activity; IEA.
CO. GO:0019039; F. Vizzal-induced cell-cell fusion; IEA.

InterPro; IPR00023; fusion_gly;
R Pfam; PR0023; fusion_gly;
R Pfam; Pfam; Pfam;
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                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
Pusion protein.
Measles virus.
Wiruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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Viruses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fusion protein.
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STRAIN-9301V;

MEDLINE-98440529; PubMed-9765410;

MEDLINE-98440529; PubMed-9765410;

Asakawa M., Nagai Y.;

Asakawa M., Nagai Y.;

Asakawa M., Nagai Y.;

Takeda M., Rato A., Kobune F., Sakata H., Li Y., Shioda T., Sakai Y.,

Asakawa M., Nagai Y.;

Takeda M., Nagai Y.;

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SEQUENCE FROM N.A.

STAIN=G954;

STAIN=G954;

MEDILINE=163526; PubMed=11773423;

A MEDILINE=2163526; PubMed=11773423;

A MAQPIATION Of Wild-type measles virus to tissue culture.";

J. Virol. 76:1505-1509(2002).

E EMBL; PQ0376; PQ0376.

R GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

GO; GO:0010939; F:viral-induced cell-cell fusion; IEA.

R GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

R HORDS : PROFONT : PROFONT : PROFONT : PER : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
45.0%; Score 72; DB 12; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
                                                                                                            Viruses, ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 LSEIKGVIVHRLEGV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                       Measles virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Measles virus
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550 AA

PRT;

PRELIMINARY;

#00% KC:#C:OT OT TOW #00

Fusion protein.

SO DR RELEASE SO DE SO DE SO DE SO DE SO DE SE DE SE DE SO D

Query Match

Matches

ò 셤 Q9YJ94 Q9YJ94;

SORRER REPORTED TO THE PROPERTY OF THE PROPERT

RESULT 13 Q9YJ94

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Gaps

.; 0

Query Match Best Local S Matches 15

à d RESULT 14 Q9QEX1

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Search completed: March 10, 2004, 09:25:31 Job time : 32.6381 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48; Search time 46.6809 Seconds

(without alignments)

Perfect score: 160
Sequence: 1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRPX 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum March 00

Maximum March 00

Maximum March 00

Fost-processing: Minimum March 00

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A Geneseq 29Jan04:*

1: geneseq11980s:*

2: geneseq11990s:*

4: geneseq22001s:*

5: geneseq22001s:*

6: geneseq22003s:*

7: geneseq22003bs:*

8: geneseq22003bs:*

Database :

SUMMARIES

	Description	Aaul1420 Synthetic	m	Aar62705 LHRH-cont	Aar62708 LHRH-cont					Add89949 LHRH pept	Aay91163 Modified	_		_	m	un.	m		Aay68582 Peptide i			0		Peptid		Aay91242 Modified
		*	*	*	7	1	7	_	~	~	7	~	~	~.	~	7	-	7	~	~	_	_				•
SUMMIES	ID	AAU11420	AAU11428	AAR62705	AAR62708	AAR62707	AAY68567	AAY91156	AAR62721	ADD89949	AAY91163	AAY91175	AAY91161	AAY91167	AAY68573	AAY91165	AAY91179	AAY91158	AAY68582	AAY91173	AAY68583	AAY91180	AAY91177	AAY68575	AAY91170	AAY91242
	DB	2	'n	7	~	4	ო	m	7	7	m	ო	٣	m	ጥ	m	ო	m	m	ო	ო	m	'n	٣	m	٣
	Length	31	47	25	42	27	27	27	45	4.5	27	31	27	27	45	45	31	28	31	31	47	47	49	27	27	35
æ	Query	99.4	99.4	73.1	73.1	72.5	72.5	72.5	72.5	72.5	70.6	68.8	67.5	67.5			6.99			65.6	65.6	65.6	65.6	64.4	64.4	64.4
	Score	159	159	117	117	. 116	116	116	116	116	113	110	108	108	108	108	107	106	105	105	105	105	105	103	103	103
	Result No.	-	6	m	4	ιυ	v	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

G	8	ã	~	159 Modif		Modifi	_			Aay68576 Peptide i	_	7 Peptide	Aay91172 Modified	Pepti	4	Peptide	8 Modifie	64 Modifie	Aay91169 Modified
2 AAR62726	2 AAR62728					m						3 AAY68577							
62.5		00 62.5 4	62.5	61.9	61.9	94 58.8 28	55.6 2	54.4 3	53.8 3	52.5		4	52.5	50.6	50.6	49.4	49.4	79 49.4 27	49.4
26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

RESU AAU1 ID	RESULT 1 AAU11420 Standard: Deptide; 31 AA. ID AAU11420 Standard: Deptide; 31 AA.
ž:	
XX	AAU11420;
i.	12-MAR-2002 (first entry)
X E	Synthetic immunogen peptide 1.
X & S	Gonadotrophin releasing hormone, GRRH; synthetic immunogen;
Z Z	nucening inthone releasing inthone, mining controlling periode epitope; promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
<u> </u>	breast cancer; uterine cancer; gynaecological cancer; endometriosis; uterine fibroid; benion prostatic hypertrophy; prostate cancer.
5 X	
SO	Measles virus.
S S	Mammalia. Sinthetic
88	Sylvinecic. Chimeric.
X P	Toy 1 field
G E.	tide
H	,
FT	Peptide 1922
닯	/not
55	Peptide ∠331 /note= "Gonadotrophin releasing hormone epitope"
1 E	
FT	notice from /note= "Amidated glycine or glycinamide"
ă	
Z S	WO200185763-A2.
\$ E	15-NOV-2001.
×	
PF	04-MAY-2001; 2001WO-US014363.
X K	05-MAY-2000; 2000US-0202328P.
X &	(APHT-) APHTON CORP.
X	
I S	Grimes S, Michaeli D, Stevens VC;
4 8	WPI; 2002-049440/06.
×	
ር ር	Novel synthetic immunogen for inducing immune response against nonadotronin releasing hormone, comprises fusion beptide having
1 6	promiscuous helper T-cell peptide epitope and immunomimic peptide epitope

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05-MAY-2000; 2000US-0202328P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR62705;
                                                  Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62705
                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
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                                                                                                                                                                                                                      ö
                                      The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH also known as lutainising hormone releasing hormone, LHRHN) comprising a fusion peptide which comprises a promiscuous helper T-cell spetide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertorphy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                  Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous helper recell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797-7
739: 47
7. Mote = "Gonadotrophin releasing hormone epitope (2-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .10 /note= "Gonadotrophin releasing hormone epitope (1. aa)"
                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= OTHER
'note= "Other= Pyro-glutamic acid or 5-oxo proline'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17. .34
/note= "Malaria CSP protein (288-302 aa)"
                                                                                                                                                                                                  Length 31;
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Amidated glycine or glycinamide"
                                                                                                                                                                                                  'Match 99.4%; Score 159; DB 5; L
Local Similarity 100.0%; Pred. No. 9.3e-17;
hes 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                        1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                             1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35. .38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .16
'note= "Spacer peptide"
                                                                                                                                                                                                                                                                                                                  AAU11428 standard; peptide; 47 AA.
                       Claim 11; Page 7; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic immunogen peptide 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2001; 2001WO-US014363
                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
aa) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200185763-A2
                                                                                                                                                                                 Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
     or its analog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia.
                                                                                                                                                                                                                                                                                                                                          AAU11428;
                                                                                                                                                                                                     Query Match
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ID AAU1
                                                                                                                                                                                                                                                                                                  RESULT 2
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The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GREH also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiseuous helper T-cell peptide epitope and useful inducing an immune response against GREH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), prostate cancer. The immunogen is effective in eliciting high and specific anti-GREH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                          Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope

    15 /note= "measles virus F protein helper T cell epitope"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; measles virus F protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

99.4%; Score 159; DB 5; Length 47;

Best Local Similarity 100.0%; Pred. No. 1.5e-16;

Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHRH-containing immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. .25
/note= "LHRH hapten"
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                                                     Stevens VC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR62705 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                     Claim 11; Page 11; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US004832.
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94US-00229275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                        Michaeli D,
(APHT-) APHTON CORP.
                                                                                                              WPI; 2002-049440/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47 AA;
                                                                                                                                                                                                                                                                      or its analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9425060-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
10-SEP-1995
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93US-00057166. 94US-00229275. 94WO-US004832

28-APR-1994; 27-APR-1993; 14-APR-1994; Zamb T;

Ladd AE, Wang CY,

(LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.

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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxia T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yershina. Spacer amino acid sequence from the invasin protein of Yershina. Spacer amino acid comains and between the immune stimulator and hapten components. When the containing, invasin-free immunogenic peptide as a above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgence for treating e.g. prostatic hyperplasia, androgence dependent carcinoma, prostatic carcinoma, testicular carcinoma, cyste, (severe) premenstrual syndrome or ostrogen-dependent breast cancer, or for induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76...30 "measles virus F protein helper T cell epitope" 733...42 //note= "LHRH hapten"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "measles virus F protein helper T cell epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; measles virus F protein.
                                                                                                                             Immunogenic luteinising hormone releasing hormone peptide(s) - that suppress LHRH activity in males and females.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 73.1%; Score 117; DB 2; Length 25; Local Similarity 85.7%; Pred. No. 1.7e-10; les 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
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                                                                                                                                                                                      Claim 8; Page 84; 213pp; English
                                                                   Zamb T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
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/note= '
                                                                                                WPI; 1994-357910/44.
                                                                   Ladd AE, Wang CY,
(LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 AA;
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10-SEP-1995
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Matches
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Gaps

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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing 5 cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide c sequence from the invasin protein of Yersinia. Spacer amino acid c sequence from the invasin protein of Yersinia. Spacer amino acid c sequence from the immune stimulator and hapten components. When the chapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component. The present sequence represents an LHRH-containing, invasin-free immunogenic peptide as above which can be used as a potent vaccine for treating e.g. protatic hyperplasia, androgence endometriosis, benign uterine tumours, recurrent functional ovarian cysts, (severe) premenstrual syndrome or oestrogen-dependent breast cancer, or for induction of infertility. (Updated on 25-MAR-2003 to

    15. 15
    /note= "measles virus F protein helper T cell epitope"
    27.
    /note= "LHRH hapten"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; lutelnising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; measles virus F protein.
                                                                                                                                                                                                                                    Immunogenic luteinising hormone releasing hormone peptide(s) - that suppress LHRH activity in males and females.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.1%; Score 117; DB 2; Length 42; Best Local Similarity 82.8%; Pred. No. 3.2e-10; Matches 24; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHRH-containing immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR62707 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                            Claim 8; Page 86; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                          WPI; 1994-357910/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
10-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Domain
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Chimeric.

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Immunogenic luteinising hormone releasing hormone peptide (s) - that suppress LHRH activity in males and females.
                                                                                                                  Claim 8, 12; Page 86; 213pp; English.
                           94WO-US004832
                                     93US-00057166
94US-00229275
                                                                                      WPI; 1994-357910/44
                                                                            Wang CY,
                                                      (LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.
      WO9425060-A1.
                          28-APR-1994;
                                     27-APR-1993;
14-APR-1994;
                 10-NOV-1994.
                                                                            Ladd AE,
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Zamb T;

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Synthetic immunogenic peptides are provided in which a universal immune slimulator is linked to a peptide or protein hapten containing B cell and cor cytotoxic T lymphocyte epitopes, giving a product which causes operent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous halper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide captured from the invasin protein of Yershina. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component sequence represents an LHRH-containing, invasin-free immunogenic peptide as above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgendence arcinoma, prostatic carcinoma, testicular carcinoma, and cysts, (severe) premenstrual syndrome or oestrogen-dependent breast cancer, or for induction of infertility. This sequence is particularly preferred. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match Nation 72.5%; Score 116; DB 2; Length 27; Local Similarity 85.7%; Pred. No. 2.7e-10; es 24; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
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Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH; luteinising hormone-releasing hormone; spermatogenesis; ovulation; ostitus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; chimera;
                                                                                                                            Peptide immunogen comprising a Th epitope and LHRH target antigen.
                              Ā
                              AAY68567 standard; peptide; 27
                                                                                               05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                    immunocastration
                                                                AAY68567;
              AAY68567
RESULT
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Measles virus Unidentified.

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The present sequence represents a peptide immunogen comprising a helper T cell (Th) epitope of the F protein of the Measles virus and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T provides optione (which is functional in genetically diverse subjects) provides optione immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (the reversible) contraceptive, control of hormone -dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IGB; anti-allergic; plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                   New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match Natch 72.5%; Score 116; DB 3; Length 27; Local Similarity 85.7%; Pred. No. 2.7e-10; les 24; Conservative 0; Mismatches 2; Indels
                                                                                                                              /note= "LHRH antigenic epitope AAY68566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:36.
                                                        "helper Th epitope AAY68540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 63; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY91156 standard; peptide; 27 AA
                                                                                             "spacer"
                                                                                                                                                                                                                                                                                                     (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                    98US-00100414.
                                                                                                                                                                                                                                 99WO-US013960.
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                                                                       .17
/note= "-
18
                                             1. .15
/note=
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                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-160562/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2003
22-MAY-2000
                                                                                                                                                                                                                                     21-JUN-1999;
                                                                                                                                                                                                                                                                      20-JUN-1998;
                                                                                                                                                                   WO9966952-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY91156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                        Wang CY;
                                          Peptide
                                                                                Peptide
                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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invention. (Updated on 12-SEP-2003 to standardise OS field)

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99WO-US013975
Measles virus.
                                                WO9966957-A2.
                                                                                                21-JUN-1999;
                                                                       29-DEC-1999
             gb.
                        Chimeric.
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UNBI-) UNITED BIOMEDICAL INC

98US-00100412.

Wang CY;

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.

Example 1; Page 77; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogenic containing them. Are used to induce a T helper cell response, containing them. Are used to induce a T helper cell response, containing them. Are used to induce a T helper cell response, containing them. The phicopes induced and or immunogenic peptides or HIV epitopes. But move generally against any pathogen, immunotenic limits them. The phicopes and containing them. The The epitopes and containing them are used for prevention and/or treatment of infunctions (HIV foot-and-mouth disease or malaria); for canetr call and peptides and the contraception, treatment of hormone (LHRH) for contraception, treatment of hormone call and peptides and peptides are acting the meat, and immunocastration) are represented a promocastration of animals or for treating libraries or created as incomparation of a promiscuous The Hilper epitope. Testing the production of animals or for treating the produces a subjects into an immunogen improves capacity or production of animals of animals or for treating to product canners and pathogen-derived Thelper epitopes. Sequence AAV91122-Y91142, AAV91226 and AAV91245-Y91246 and AAV91245-Y91246 animal and sequences AAV91122-Y91142, AAV91226 and AAV91245-Y91246 animal and sequences AAV91122-Y91144, AAV9126 and AAV91245-Y91246 animal an

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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or syrbtoxaxt Tlymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator respensents an LHRH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19. .33
/note= "measles virus F protein helper T cell epitope"
36. .45
                                                      Gaps
                                                                                                                                                                                                                                                                                                                         Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; measles virus F protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic luteinising hormone releasing hormone peptide(\epsilon) - that suppress LHRH activity in males and females.
                                                      5
                           Length 27;
                       Score 116; DB 3; Length 27
Pred. No. 2.7e-10;
0; Mismatches 2; Indels
                                                                                    3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                           1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .16
/note= "invasin domain"
                                                                                                                                                                                                                                                                                               LHRH-containing immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "LHRH hapten"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                          AAR62721 standard; peptide; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US004832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00057166.
94US-00229275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ladd AE, Wang CY, Zamb T;
                                                                                                                                                                                                                                                    (revised)
(first entry)
                            Query Match
Best Local Similarity 85.7°
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-357910/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.
Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9425060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1994;
                                                                                                                                                                                                                                                    25-MAR-2003
10-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                       AAR62721;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                               RESULT 8
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The present sequence is that of a synthetic immunogenic peptide derived from human LHFH. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as advant and as peptide immunogen stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogen. The complex is particulate and contropoduce an immune response. The complexes may be prepared with various for produce an immune system to produce an immune size of the microparticle. An immunostimulatory complex comprising the present LHRH derived peptide can be used in a vaccine for prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHRH peptide used in immunostimulant complex for prostate cancer vaccine.
containing immunogenic peptide as above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-dependent carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis, benign uterine tumours, recurrent functional ovarian cysts, (severe) premenstrual syndrome or osstrogen-dependent breast cancer, or for induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulant; vaccine; human; immunogen; LHRH; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 7; Length 45;
Pred. No. 5e-10;
0; Mismatches 2; Indels
                                                                                                                                                                         Length 45;
                                                                                                                                                                                                             2; Indels
                                                                                                                                                                         .;
73
                                                                                                                                                                       Query Match 72.5%; Score 116; DB 2;
Best Local Similarity 85.7%; Pred. No. 5e-10;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                 3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                     19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO 9; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    ADD89949 standard; protein; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2002; 2002US-00076674. 31-JAN-2003; 2003US-00076674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2003; 2003WO-US004711
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003068169-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer
                                                                                                                                      Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sokoll KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                        ADD89949;
                                                                                                                                                                                                                                                                                                                                              RESULT 9
ADD89949
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The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention and immunogenic peptides comprising the Th epitopes of the invention and peptide immunogens containing them, are used to induce a T helper cell response, protein (ETFP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tunour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIRW) for contraception, treatment of hormone releasing hormone (LHRM) for ontraception, treatment of hormone releasing hormone (LHRM) for ontraception, treatment of hormone releasing hormone and provents of an immunogens improves capacity to arreriosclerosis. Incorporation of a promiscuous Th (functional in production of antibodies against a target antigen. Th can replace carrier production of antibodies against a target antigen. Th can replace carrier protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 represents a promiscuous Thelper epitope from the meaales virus (MVF) protein and sequences AAY91144-Y91155 are synthetic epitopes auriace antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91277 and AAY9124-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
                                                                                                                                                                                                                                                                                                                       Promiscuous T-cell epitope, measles virus F protein; MVF; hepatitis B Virus surface antigon; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic; plasmodium falciparum; circumsporcozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:43.
  30
                                       4
                              19 LSEIKGVIVHRLEGVGGE--HWSYGLRP
3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 80; 129pp; English
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                                                                                                                                             AAY91163 standard; peptide; 27
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Measles virus
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22-MAY-2000
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                                                                                                                                                                                  AAY91163;
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Gaps

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CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide target antigenic peptides. AAY91200 is sometostatin, and these LHRH antigenic peptides. AAY91201 sometostatin, and the epitope. Sometostatin immunogens may be used to promote growth in the princip of the prevent HV infection of T cells. AAY90212 is a modified with the pitope/CD4 CDR2 antigenic peptides which may be used to prevent HV infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/GPG CH3 antigenic peptides which may be used in the creatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VPI capsid protein and AAY91221-Y9122 comprise this corrumsporcacite (CS) target antigen, and AAY91221-Y91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91221 represent CETP-derived peptides and AAY91223-Y91241 are immunogens comprising a CETP-derived peptides and AAY91224-Y91240 are immunogens comprising a CETP-perived peptides and AAY91224-Y91240 are immunogens comprising a CETP-derived peptides and AAY91229-Y91241 are conformed to treat arteriosclerosis and cardiovascular disease. AAY91240-Y91251 are antigenic peptides comprising MVH Th and CY91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and CC HIV-1 B-cell epitope which may be used as a component in an anti-HV-1 convection epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 27. AA;

Gaps 70.6%; Score 113; DB 3; Length 27; 82.1%; Pred. No. 7.7e-10; ive 1; Mismatches 2; Indels 3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30 1 LSEIKGVIVHKLEGVGGE--HWSYGLRP 26 23; Conservative Query Match Best Local Similarity Matches 23; Conserv ò g

AAY91175 standard; peptide; 31 AA. (revised)
(first entry) Modified MVF 12-SEP-2003 22-MAY-2000 AAY91175; RESULT 11 AAY91175 ID AAY

Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; sometostatin; growth promotion; CD4 receptor; HIV-I; antiviral; FMDV; foct and mouth disease virus; immunoglobulin B; IgB; anti-allergic; Plasmodium falloiparum; circumsporcozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic. Th epitope/LHRH antigenic peptide, SEQ ID NO:55.

Measles virus. WO9966957-A2 29-DEC-1999, Chimeric.

98US-00100412. 21-JUN-1999; 20-JUN-1998; UNBI-) UNITED BIOMEDICAL INC

Wang CY;

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.

Example 1; Page 84; 129pp; English

The invention relates to novel promiscuous T helper cell epitopes (Th),
along with B cell epitopes. The Th epitopes and peptide immunogenic peptides comprising the The epitopes and peptide immunogenic peptides. The Th epitopes and peptide immunogenic pecifically against Planmachium falciparum, cholesteryl ester transport containing them, are used to induce a T helper cell response, specifically against Planmachium falciparum, cholesteryl ester transport correlating telminogens may be used for prevention and/or treatment of infections [HIV] foot-an-mouth disease or malaria); for cancer immunotent prevention of the action of lutefinisting hormone infections [HIV] foot-and-mouth disease or malaria); for cancer immunotent prevention of promiserous The functional in the contraception, treatment of hormone (LHM) for contraception, treatment of hormone infections [HIV] foot-and-mouth disease or malaria); for cancer relations of promiserous Theorems and performed and action of lutefinishing hormone corrections and sequenced prevent of animals; or for treating allergies or recipied diverse subjects) into an immunogen improves capacity to production of antibodies against a target antidem. The canterioral progress are promiserous a promiserous and pathogened derived T helper cell mediated manual sequence any production of antibodies against a target antidem. The canterior profuser of antibodies against a large antidem. The canterior corresponds and Advised *Yavist (HWY) process and performed and sequence Advised to product on an action of antibodies against a large antidem. Advised and Advised *Yavist (HWY) process antigent opptides comprising sometostatin and sequence Advised *Advised *Advised

Sequence 31 AA;

Gaps . 0 68.8%; Score 110; DB 3; Length 31; 78.6%; Pred. No. 2.6e-09; ive 1; Mismatches 5; Indels 1; Mismatches 22; Conservative Similarity Query Match Best Local S Matches

3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30

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3 LSEIKGVIVHKLEGVLFGGEHWSYGLRP AAY91161 standard; peptide; 27 AA AAY91161; RESULT 12 AAY91161 g

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Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgE; anti-allergic; plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                          Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNBI-) UNITED BIOMEDICAL INC
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                              Measles virus.
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12-SEP-2003
22-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
Chimeric.
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The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
and immunogenic peptides comprising the Th epitopes and peptide immunogens
containing them, are used to induce a Thelper cell respones.
Specifically against Plasmachium falciparum, cholesteryl ester transport
protein (CETP) or HIV epitopes, but more generally against any pathogen,
immunoreactive self-antigen or tumour antigen. The Th epitopes and
immunoreactive self-antigen or tumour antigen. The Th epitopes and
immunoreactive self-antigen or tumour antigen. The Th epitopes and
immunoreactive self-antigen or tumour antigen. The Th epitopes and
immunoreactive self-antigen or tumour antigen. The Th epitopes and
immunoreactive self-antigen or tumour antigen. The Th epitopes and
celepandent cancer, prevention of boar taint in meat, and immunocasization)
celepandent cancer, prevention of boar taint in meat, and immunocasization)
creleasing hormone (LHEM) for contrareaction, treatment of hormone
releasing hormone (LHEM) for contrareaction of a promiscuous Th (functional in
carteriosclerosis. Inocoporation of a promiscuous Th (functional in
contrared the growth of animals, or for treatment of hormone
contrared the promiscuous Thelper epitopes. Sequence AAY9112,
contrared antigences AAY9112-Y9114, AAY91226 and AAY9122,
crepresents a promiscuous Thelper epitopes from the measles virus F (MVF)
crepresents a promiscuous Thelper epitopes from the measles virus (
cused in these LHRH antigenic peptides comprising sometostatin, and
carigenic peptides comprising and AAY91220
cused in these LHRH antigenic peptides comprising sometostatin, and
contrared from the prope (CD4 CDR2-11ke domain antigenic and
contrared from the proper AAY91197 is the LHRH target antigenic mappetides comprising sometostatin and
cused in these LHRH antigenic peptides comprising sometostatin and
contrared to prevent HIV infection of T cells. AAY91201 is a modified
contrared to prevent HIV infection of T cells and AA New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis Example 1; Page 79; 129pp; English antigenic site, for immunization e or human immune deficiency virus.

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disease virus (FMDV) VP1 capsid protein and AAV91221-Y91222 comprise this peptide and a Th epitope. AAY9123 is a plasmodium falciparum circumsporzocite (CS) target antigen, and AAAV91225 comprise the CS antigen and an WVF Th epitope and may be used in a malaria vaccine. AAV91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a CTP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91199 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatcostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic; plasmodium falcipatum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel promiscuous T helper cell epitopes (Th) and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response,
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 71.4%; Pred. No. 4.4e-09;
as 20; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promiscuous T-cell epitope; measles virus F protein; MVF;
                                                                                                                                                                                                                                                                                                                                                                                                             3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ISEIKGVIVHKIEGIGGE--HWSYGLRP 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY91167 standard; peptide; 27
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(first entry)
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                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
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22-MAY-2000
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY91167
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Synthetic. Yersinia sp. Measles virus. Unidentified.

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specifically against Plasmodium falciparum, cholesteryl ester transport crock specifically against Plasmodium falciparum, cholesteryl ester transport cortein (CETP) or HIV epitopes, but move generally against any pathogen, immunoceactive self-antigen or tumour antigen. The The epitopes and perpide immunoceactive self-antigen or tumour antigen. The The pitopes and perpide immunoceactive inhibition of the action of luteinising hormone caleasing hormone (LHEM) for contraception, treatment of hormone releasing hormone (LHEM) for contraception, treatment of hormone caleasing hormone (LHEM) for contraception, treatment of hormone caleaning the growth of a promiscuous The legal antigon of antipodes against a target antigon of antipodes against a target antigon. Beatled immune response, resulting in protein and sequences AAV91122-V91143, AAV91226 and AAV91245-V9124 for protein and sequences AAV91144, AAV91126 and AAV91245-V91246 cortises and sequences based on the WFF The pitope Sequence AAV91141 represents a promiscuous The pitope based on the WFF The pitope Sequence AAV91144 v991156 are synthetic epitopes Genical and sequences and AAV91126 and AAV9124 and sequence of the pitope Comprising and antigent of periode antigenic peptides comprising somatostatin and promiscuous The apitope AAV91144 v991156 and AAV9124 and AAV9124 are antigenic peptides comprising somatostatin and antigenic peptides which may be used to promit of a human IgE (Ammunoglobulin B) (H3 domain, and AAV9121-9) and mouth antigen and and antigenic peptides which may be used to promit of a human IgE (Ammunoglobulin B) (H3 domain antigenic peptides and and ant peptides AAV9125 at a peptide derice of a proper of a proper of a proper of

Sequence 27 AA;

Gaps 7 67.5%; Score 108; DB 3; Length 27; 75.0%; Pred. No. 4.4e-09; ive 3; Mismatches 2; Indels Query Match Best Local Similarity 75.0° Matches 21; Conservative

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3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30

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AAY68573 standard; peptide; 45 AA. AAY68573 RESULT &&&&&&&&XBXBXXXXX

AAY68573;

05-MAY-2000 (first entry)

Peptide immunogen comprising a Th epitope and LHRH target antigen.

Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH; luteinising hormone-releasing hormone; spermatogenesis; ovulation; oestrus; sexual development; sex hormone; promiscuous T helper epitope; vectine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; invasin domain; immunocastration.

The present sequence represents a peptide immunogen comprising an invasin domain immunostimulatory peptide of Yersinia sp., a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The synthetic Th epitope is derived from a structured synthetic antigen library (SSAL) designated SSAL1 Thl is synthetic antigen library (SSAL) designated SSAL1 Thl is shouthet a promiscouse epitope taken from the Protein of the Measles virus. The peptide immunogens cause induction of a specific immune response to IHRH which is involved in regulation of specific immunogens, ovulation, oserrus, sexual development and secretion of spermatogenesis, ovulation, oserrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis), to prevent boar taint (and improve meat quality) and for immunocastration New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer. 36. .45 /note= "LHRH antigenic epitope AAY68566" . .16 note= "invasin domain AAY68565" Location/Qualifiers Claim 9; Page 71; 102pp; English. 34. .35 /note= "spacer" "spacer" (UNBI-) UNITED BIOMEDICAL INC 98US-00100414. 99WO-US013960. 17. .18 /note= WPI; 2000-160562/14. Sequence 45 AA; 21-JUN-1999; 20-JUN-1998; WO9966952-A1 29-DEC-1999. Wang CY; Peptide Peptide Peptide Peptide Peptide

Query Match 67.5%; Score 108; DB 3; Length 45; Best Local Similarity 71.4%; Pred. No. 8.2e-09; Matches 20; Conservative 4; Mismatches 2; Indels 3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30

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19 ISEIKGVIVHKIEGIGGE--HWSYGLRP 44 RESULT 15

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AAY91165 standard; peptide; 45 AAY91165

AAY91165;

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12-SEP-2003 22-MAY-2000

Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:45

(revised)
(first entry)

Promiscuous T-cell epitope, measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic; plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.

Measles virus. Rattus sp. Chimeric.

WO9966957-A2

29-DEC-1999.

99WO-US013975 21-JUN-1999;

98US-00100412 20-JUN-1998; (UNBI-) UNITED BIOMEDICAL INC

Wang CY;

WPI; 2000-160564/14

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.

Example 1; Page 80; 129pp; English

The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
and immunogenic peptides comprising the Th epitopes of the invention
and immunogenic peptides. The The pitopes and peptide immunogens
containing them, are used to induce a Thelper cell response,
containing them, are used to induce a Thelper cell response,
containing them, are used to induce a Thelper cell response,
containing them, are used to prevention and/or treatment of
immunocactive self-antigen or tumour antigen. The Th epitopes and
immunocactive self-antigen or tumour antigen. The Th epitopes and
confections (HIV) foot-and-mouth disease or malaria); for cancer
immunotherapy; for inhibition of the action of luteinising hormone
releasing hormone (LHRH) for contraception, treatment of hormone
releasing hormone (LHRH) for contraception, treatment of hormone
releasing hormone (LHRH) for contraception, treatment of hormone
contractions (HIV) for inhibition of boar taint in meat, and immunocastration)
carteriosclerosis. Inocropration of a promiscuous Th (functional in
carteriosclerosis. Inocropration of a promiscuous Th (functional in
carteriosclerosis. Inocropration of a promiscuous Th (functional in
contraction of antibodies against a target antigen. Th can replace carrier
contraction of antibodies against a target antigen. The can replace carrier
contraction of antibodies against a target antigen. The market (HIV)
contraction of antibodies against a target antigen. Fortunes
contraction and sequences ANY91122-Y91142, ANY91225 and AAY91245
corpresents a promiscuous Th epitope from the measles virus (MIV)
corpresents antigenic applicate (THRH target antigenic peptides
corpresent synthetic The Publication of ANY912012 and ANY912012
corpresents antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91201 as antigenic peptides comprising an LHRH sequence joined to a human IgE (Immunoglobulin E) Gals domain antigenic antigenic peptides of a human

peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporzotice (CS) target antigen, and AAAY91224-491225 comprise the CS antigen and an AAY91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY9124 and AAY9125-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 are antigenic peptides comprising WVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91199 and AAY91199 are respectively an immunostimulatory both of which may optionally be used in the antigenic peptides spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field) %\$

Sequence 45 AA;

Gaps 5 Length 45; Query Match
Best Local Similarity 71.4%; Pred. No. 8.2e-09;
Matches 20; Conservative 4; Mismatches 2; Indels

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Search completed: March 10, 2004, 09:12:09 Job time : 47.6809 secs

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Wed Mar 10 10:34:3/ 2004
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: March 10, 2004, 09:16:59; Search time 4.71595 Seconds

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268.645 Million cell updates/sec

Perfect score: 29
Sequence: 1 SSGPSL 6
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742
Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 6, Appli	Sequence 7, Appli	Sequence 15, Appl	Sequence 13, Appl	Sequence 16, Appl	Sequence 14, Appl	Sequence 19, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 20, Appl	Sequence 47649, A	Sequence 425, App	Sequence 425, App	Sequence 38, Appl	Sequence 38, Appl
ID	US-09-848-834A-6	US-09-848-834A-7	US-09-848-834A-15	US-09-848-834A-13	US-09-848-834A-16	US-09-848-834A-14	US-09-848-834A-19	US-09-848-834A-17	US-09-848-834A-18	US-09-848-834A-20	US-09-864-761-47649	US-09-731-872-425	US-09-876-997-425	US-09-870-756-38	US-09-874-585B-38
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Score	29	29	29	50	29	53	29	29	29	53	29	59	50	50	29
Result No.		71	m	4	ιυ	φ	7	60	on	10	11	12	13	14	15

Seguence 9393, Ap	Sequence 6493, Ap	Sequence 34, Appl	Sequence 38, Appl	equence 36	4,			7	Ñ	ø	•	Sequence 28, Appl	Sequence 46, Appl	•	•	٠.	•	٠.	ednence,	equence	•	Sequence 26, Appl	•	٠,	٠.	٠.	_	Sequence 49, Appl	4
US-10-156-761-9393	738-626	-210-13	-210-130	-210-	-379-381	5 US-10-379-381-2	-764-89	1 US-10-225-567A-438	196	-977-41	977-4	US-09-977-03	US-09-977-033A	-977	977-751C-4	9-776	977-639A-4	-977-819B-2	977-8		-10-145-58	-41	-977-0	-977-751C-2	-977-6	S-09-977-	828-36	09-909-320	US-09-909-088B-49
2 14	7	6 15	8 15	2 15	2 15	8 15	2 10	6 14	n o	5 10	5 10	+4	5 10	5 10	5 10	5 10	5 10	5 11	5 11	5 14	5 14	3 10	3 10	3 . 10	3 10	•	•	o 6	•
49	1197	318	320	325	326	326	12	9	64	64	64	645	64	64	64	64	64	64	64	64	64	9	9	99	9	9	60	69	69
100.0	100.0	100.0	100.0	100.0	100.0	100.0	93.1	93.1	m			93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1
53	53	53	53	53	53	53	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
16	17	18	19	20	21	22	23	24	25	26	27	28	,59	30	31	32	33	34	35	36	37	38	e O	40	41	42	.43	44	45

ALIGNMENTS

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US-09-848-834A-6

Sequence 6, Application US/09848834A

Sequence 6, Application US/09848834A

Serent No. US20020076416A1

GENERAL INFORMATION:
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: 60/202,326

PRIOR APPLICATION NUMBER: 60/202,326

PRIOR APPLICATION NUMBER: 60/202,326

NUMBER OF SEQ ID NOS: 20

SEQ ID NOS: 20

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin 3.0

SOFTWARE: P
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Gaps

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TYPE: PRI
TYPE: PRI
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
ORGANISM:
PEATURE
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the C
OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of
OTHER INFORMATION: Hhormone linked by a spacer to amino acid sequence 288-302 of
OCHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KEY: PEPTIDE
OCHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
OCHER INFORMATION: Spacer peptide
OTHER INFORMATION: Amino acid sequence 288-302 of the Measles
OTHER INFORMATION: Amino acid sequence 288-302 of the Measles
OTHER INFORMATION: Virus fusion protein, F
OCHER INFORMATION: Virus fusion protein, F
OCHER INFORMATION: No VIRUS
OTHER INFORMATION: No VIRUS FRES
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LOCATION: (1)...(1)
OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
LOCATION: (1)...(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GRRH hormone
LOCATION: (1)...(16)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COTHER INFORMATION: Pyroglutamic acid or 5-oxoproline US-09-848-834A-13
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US-09-848-834A-16
US-09-848-834A-16
Sequence 16, Application US/09848834A
Fequence 16, Application US/09848834A
Federic No. US20020076416A1
FEDERICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REPRENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
FRIOR RAPPLICATION NUMBER: 60/202,328
FRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 36
            GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION:
CURRENT PELLING DATE: 1002865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT PILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEC ID NO 13
LENGTH: 34
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 6; Conservative
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NAME/EXE: MODERES
LOCATION: (1)...(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
NAME/EXE: PEPTIDE
LOCATION: (1)...(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/EXE: PEPTIDE
LOCATION: (11)...(16)

OTHER INFORMATION: Spacer peptide
NAME/EXE: PEPTIDE
LOCATION: (17)...(31)

OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor
OTHER INFORMATION: (Tentoxylysin)
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100.0%; Score 29; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Aphton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102685-004

FURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.0

SEG ID NO 15

LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 29; DB 9; I
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0;
                     CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 8
                                                                                                                                                                                                                                                                                                    PEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-848-834A-7
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US-09-848-834A-13
; Sequence 13, Application US/09848834A
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FILE REFERENCE: 1102865-0047
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PEATURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of huma
OTHER INFORMATION: GARH linked by a spacer to amino acid sequence 830-844 of Tetan
OTHER INFORMATION: toxoid precursor (Tentoxylysin) linked by a spacer to amino aci
OTHER INFORMATION: sequence 1-10 of GARH
NAME/EXY: MOD_RES.
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RH hormone linked by a spacer to amino acid sequence 288-30
the Messles virus protein F linked by a spacer to amino aci
wence 2-10 of the GRPH hormone
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Patent No. US20020076416A1

GENERAL INFORMATION

APPLICATION COLPORATION

TITLE OF INVENTION Chimeric Peptide Immunogens

FILE REFRENCE: 1120865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT PILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR PILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 17

LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 29; DB 9; I 100.0%; Pred. No. 1.1e+02; rative 0; Mismatches 0;
      60/202,328
PRIOR APPLICATION NUMBER: 60/202
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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OTHER INFORMATION: UI
OTHER INFORMATION: UI
OTHER INFORMATION: UI
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: PI
NAME/KEY: MOD_RES
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US-09-848-834A-17
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NAMELKEY: MOD RES
NAMELKEY: MOD RES
NAMELKEY: PEPTIDE
NAMELKOY: PEPTIDE
NAMELKOY: PEPTIDE
NAMELKEY: PEPTIDE
NAMELKEY: PEPTIDE
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NAMELKEY: PEPTIDE
NAMELKEY: PEPTIDE
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; OTHER INFORMATION: Amino acid sequence 947-967 of the Tetanus toxoid precursor; OTHER INFORMATION: (Tentoxylysin)
US-09-848-834A-14
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                            9; Length 36;
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Patent No. US2002076416A1
GENERAL INFORMATION:
JETLE AINTERPRESSION COMPORATION:
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-004
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR APPLICATION NUMBER: 60/202,328
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.0
SEQTIVANCE: 37
LENGTH: 37
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Patent No. US20020076416A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REPERBUCE: 1102865-0047
CURRENT APPLICATION WIMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
                                                                                                                                                              99;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                              100.0%; Score 29; 100.0%; Pred. No. 8
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OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
                                                                                                                                                                                                     .
              OTHER INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                  Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 6; Conserv
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US-09-848-834A-19
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PERALUKE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human OTHER INFORMATION: GARH linked by a spacer to amino acid sequence 378-398 of Plasmc OTHER INFORMATION: ium falciparum circumsporozoite (CSP) protein
NAMB/KRY: MOD_RES
NAMB/KRY: MOD_RES
NAMB/KRY: MOD_RES
NAMB/KRY: MOD_RES
NAMB/KRY: MOD_RES
NAMB/KRY: PEPTIDE
LOCATION: (1)...(10)
OTHER INFORMATION: Amidated glycine or glycinamide
NAMB/KRY: PEPTIDE
LOCATION: (1)...(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GARH hormone
NAMB/KRY: PEPTIDE
LOCATION: (11)...(16)
OTHER: INFORMATION: Amino acid sequence 1-10 of the human GARH hormone
NAMB/KRY: PEPTIDE
LOCATION: (11)...(16)
OTHER: INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATION: (17)...(36)
COTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum OTHER INFORMATION: circumsporozoite (CSP) protein
NAME/KEY: PEPTIDE
COCATION: (37)...(42)
COTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (43)...(51)
COTHER INFORMATION: Amino acid sequence 2-10 of the human GRRH hormone US-09-848-834A-20
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                       Length 50;
                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/09848834A

Patent No. US20020076416A1

GENERAL INPORMATION:

APPLICANT: Aphton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-004

FURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR PILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SEQ ID NOS: 20

SEQ ID NOS: 20

LENGTH: 51
                                    100.0%; Score 29; DB 9; 100.0%; Pred. No. 1.2e+02;
                                                                                        0; Mismatches
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Sequence 47649, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                         US-09-848-834A-20
US-09-848-834A-18
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  LOCATION: (47)...(47)

OTHER INFORMATION: Amidated-glycine or glycinamide

NAME/KEY: PEPTIDE

LOCATION: (1)...(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

LOCATION: (11)...(18)

OTHER INFORMATION: Spacer peptide

LOCATION: (19)...(34)

OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein,

NAME/KEY: PEPTIDE

LOCATION: (35)...(38)

OTHER INFORMATION: Spacer peptide

LOCATION: (35)...(38)

OTHER INFORMATION: Spacer peptide

LOCATION: (35)...(47)

OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human OTHER INFORMATION: GRAH linked by a spacer to amino acid sequence 947-967 of the Tet OTHER INFORMATION: anus toxoid precursor (Tentoxylysin) protein linked by a spacer to OTHER INFORMATION: o amino acid sequence 2-10 of human GRAH
NAMPINEN: MOD RES
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LOCATION: (42)..(50)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GRRH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 47;
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REPERENCE: 110286-20047
CURRENT APPLICATION UNMER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMERE: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-848-834A-18
Sequence 18, Application US/09848834A
Patent No. US20020076416A1
GENERAL INFORMATION:
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INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 SSGPSL 16
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LENGTH: 50
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Sequence 425, Application US/09876997

Publication No. US2030152921A1

GENERAL INPORMATION:

APPLICANT: Dougueleret, Lydie

APPLICANT: Doubert, Severin

APPLICANT: Bougueleret, Lydie

APPLICANT: Dobert, Severin

TILE OF INVEXTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US4.CIP

CURRENT APPLICATION NUMBER: US/0976,997

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-07

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

SOFTWARE: PATENT PM
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: JODGET, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.U53.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT PILLING DATE: 2000-12-07
PRIOR PILLING DATE: 1999-12-08
PRIOR PILLING DATE: 1999-12-08
PRIOR PILLING DATE: 2000-3-06
NUMBER OF SEQ ID NOS: 482
SSOFTWARE: PATENT 
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Sequence 38, Application US/09870756
Patent No. US20020052023A1
GENERAL INFORMATION:
APPLICANT: VITTANEN, PAUL VEIKKO
BACOT, KAREN CNLEY
JORDAN, DOUGLAS BRIAN
TITLE OF INVENTION: RIBOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 SSGPSL 46
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APPLICANT: CHEN, WENTERS, DAYLO A.
TITLE OF INVENTION: HENDA GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL
CTREARY PAPELICATION NUMBER: US/09/864,761
GREARY PAPELICATION NUMBER: US/09/864,761
FRIOR APPLICATION NUMBER: US/09/864,761
FRIOR PAPELICATION NUMBER: US/09/864,761
FRIOR PAPELICATION NUMBER: US/09/864
FRIOR APPLICATION NUMBER: US/09/966
FRIOR APPLICATION NUMBER: US/09/964
FRIOR PAPELICATION NUMBER: US/09/964
FRIOR PAPELICATI
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CTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 0.96
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.57
CTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.67
CTHER INFORMATION: SWISSPROT HIT: 052399, EVALUE 5.90e+00
CTHER INFORMATION: EST_HUMAN HIT: AAB13575.1, EVALUE 3.00e-22
US-09-864-761-47649
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Patent No. US20020102604A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP T
OTHER INFORMATION: EXPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 6; Conserv
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US-09-731-872-425
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APPLICANT: Voitanen, Paul Veikko;
APPLICANT: Jordan, Douglas Brain
APPLICANT: Bacci, Karen Onley;
TITLE OF INVENTION: Riboflavin Synthase Genes and Enzymes and Methods of Use;
TITLE OF INVENTION: Riboflavin Synthase Genes and Enzymes and Methods of Use;
TITLE OF INVENTION: Riboflavin Synthase;
CURRENT APPLICATION NUMBER: US/09/874,585B
CURRENT PILING DATE: 2002-03.5
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE Microsoft Office 97
SEQ ID NO 38
LINGTON OF SEQ ID NOS: 39
LINGTON OF SEQ ID NOS: 39
LINGTON OF SEQ ID NOS: 39
LINGTON OF SEQ ID NOS: 30
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0
                                      CURRESPONDENCE AULDESS:
CURRESPONDENCE AULD COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAMARE
STATE: DELAMARE
STATE: DELAMARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: MICROSOFT WORD VERSION 7.0A
APPLICATION DATE: 3.609/870,756
FILING DATE: 31-May-2001
CLASSIFICATION NUMBER: US/09/870,756
FILING DATE: 31-May-2001
CLASSIFICATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1083
TELECOMMUNICATION: CHANGER: CL-1083
TELECOMMUNICATION: CANAGETIVE
METERSPECIAL NUMBER: CL-1083
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100.0%; Score 29; DB 9; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 38: US-09-870-756-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 200 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/09874585B Patent No. US20020127670A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 302-992-8112
TELEPAX: 302-773-0164
INFORMATION FOR SEC ID NO: 38:
SEQUENCE CHARACTERISTICS:
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     NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 SSGPSL 84
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US-09-874-585B-38
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Search completed: March 10, 2004, 10:25:47 Job time : 4.71595 secs
1 SSGPSL 6
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March 10, 2004, 08:58:48; Search time 9.03502 Seconds (without alignments) 187.635 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Database :

SUMMARIES	Description	1417 Aaul1417 Synthetic	8 Aau11418	26 Aau11426	24 Aau11424	7 Aau11427	5 Aau11425	0 Aau11430	8 Aau11428	9 Aau11429	47 Aag03447	Aau11431	Aam18164	Abb37195	Aam70325	v	5 Aag89305 Human	N54 Aaol0754 Human pol	1 Aay73871 Human	3 Aau42353	3872 Propionib	2 Aau30732	5 Abg19555	6 Abg1955	۳	00000
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Gonadotrophin releasing hormone; GnRH; synthetic immunogen; luteinising hormone releasing hormone; LHRH; contraceptive; promiscuous helper T-cell peptide epitope; immunomimic peptide epitope; breast cancer; uterine cancer; gynaecological cancer; endometriosis; uterine fibroid; benign prostatic hypertrophy; prostate cancer; AAU11417 standard; peptide; 6 AA Synthetic spacer peptide #2 (first entry) spacer peptide 12-MAR-2002 AAU11417;

04-MAY-2001; 2001WO-US014363. 05-MAY-2000; 2000US-0202328P. (APHT-) APHTON CORP. WO200185763-A2. 15-NOV-2001. Synthetic.

Stevens VC; Ď, Michaeli Grimes S,

WPI; 2002-049440/06.

Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.

Claim 10; Page 6; 43pp; English.

The invention relates to a synthetic immunogen for inducing specific antibodies against gonadorropin releasing hormone (GRMH also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiseuous helper T-cell peptide epitope and immunose helper T-cell peptide epitope and immunose response against GRMH in an animal subject, and as such is useful inducing as contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer),

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Gaps

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Indels

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Mismatches

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luteinising hormone releasing hormone; LiRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer;
endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GARH antibody titres. The present sequence is a synthetic spacer peptide used in the immunogen of the invention
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 6, Conservative
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Best Local Similarity
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The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GRRH also known as lutainising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GRRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GRRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
                                                                                                                                                                                                                              Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
luteinising hormone releasing hormone; iHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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/note= "Tetanus toxoid sequence (830-844 aa)"
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/note= "Spacer peptide"
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                                                                                                          AAU11426 standard; peptide; 31 AA.
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                                                                                                                                                                                                   Synthetic immunogen peptide 7.
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                                                                                                                                                                     12-MAR-2002 (first entry)
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Synthetic.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel synthetic immunogen for inducing immune response against pronadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
                                                                                                                                                                                                                                                                                    Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
luteinishing hormone releasing hormone; LHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= OTHER
/note= "Other= Pyro-glutamic acid or 5-oxo proline"
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'note= "Gonadotrophin releasing hormone epitope"
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/note= "Measles virus fusion protein F epitope"
                        100.0%; Score 29; DB 5; Length 31; 100.0%; Pred. No. 85; o; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                            Synthetic immunogen peptide 5.
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             Query Match
Best Local Similarity 100.
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 Sequence 31 AA;
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Synthetic.
Chimeric.
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prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                      Gonadotrophin releasing hormone; GnPH; synthetic immunogen;
luteinising hormone releasing hormone; LHFH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
                                                                                                                            Gaps
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/note= "Other= Pyro-glutamic acid or 5-oxo proline"
11. .16
/note= "Spacer peptide"
17. .36
/note= "Malaria CSP protein (378-398 aa)"

    10 'note= "Gonadotrophin releasing hormone epitope"

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                                                                                                                                                                                                                                                                                                                                                            Synthetic immunogen peptide 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
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Synthetic.
Chimeric.
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Peptide
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useful inducing an immune response against GRRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GRRH antibody titres. The present sequence is a synthetic immunogen of the invention
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luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous heiper re-cell peptide epitope; immunominic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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'note= "Other= Pyro-glutamic acid or 5-oxo proline"
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/note= "Gonadotrophin releasing hormone epitope"
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                                                                                                                                         Length 36;
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                                                                                                                                                                  0; Indels
                                                                                                                                          2
                                                                                                                                   DB .
                                                                                                                                                                    Mismatches
                                                                                                                                         Score 29;
Pred. No.

    11. .16
    /note= "Spacer peptide"
    17. .37

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                                                                                                                                                                                                                                                                                                AAU11425 standard; peptide; 37 AA
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0
                                                                                                                                         100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic immunogen peptide 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2001; 2001WO-US014363
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                1 SSGPSL 6
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                                                                                                                Sequence 36 AA;
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Synthetic.
Chimeric.
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Peptide
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antibodies against gonadotropin releasing hormone (GnRH also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promisectuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Gonadotrophin releasing hormone epitope (2-10
                                                                                                                                                                                                               Gaps

    10 'note= "Gonadotrophin releasing hormone epitope (1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or 5-oxo proline"
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                                                                                                                                                                                     Length 37;
                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aa)
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                                                                                                                                                                                    Score 29; DB 5;
Pred. No. 1e+02;
Mismatches 0
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:e= "Spacer peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  AAU11430 standard; peptide; 46 AA
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                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2001; 2001WO-US014363
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                                                                                                                                                               Sequence 37 AA;
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Synthetic.
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Michaeli D,

Grimes S,

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AAU11428 standard; peptide; 47 AA
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Matches 6; Conservative
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                                                         WPI; 2002-049440/06
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Synthetic.
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The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH also known as futerinishing hormone releasing hormone, LiBHP) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                    Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
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luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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/note= "Amidated glycine or glycinamide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 11; 43pp; English.
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                                                                                                                             04-MAY-2001; 2001WO-US014363.
                                                                                                                                                                    05-MAY-2000; 2000US-0202328P
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Best Local Similarity luv...
G; Conservative
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                                           WO200185763-A2
                                                                                                                                                                                                                                                                                                                                                                                                             or its analog
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                                                                                  15-NOV-2001
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Synthetic.
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                                                                                                                                                                                                                             The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH also known as fluteinishing hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometricals, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                  Novel synthetic immunogen for inducing immune response against
gonadotropin releasing hormone, comprises fusion peptide having
promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gonadotrophin releasing hormone; GnPH; synthetic immunogen;
luteinising hormone releasing hormone; iHRH; contraceptive;
promiscuous helper r-cell peptide epitope; immunomimic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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47
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1. 10
//note= "Gonadotrophin releasing hormone epitope (1. aa)"
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/note= "Other= Pyro-glutamic acid or 5-oxo proline"
| 11 16 /note= "Spacer peptide"
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17. .34
/note= "Malaria CSP protein (288-302
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/note= "Spacer peptide"
39. .47
  Stevens VC;
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Gaps

Peptide Peptide Peptide Peptide

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The present sequence is a polypeptide encoded by one of a large number of s. ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA perimed cDNA libraries show been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gonadotrophin releasing hormone; GnRH; synthetic immunogen; luteinising hormone releasing hormons; LHRH; contraceptive; promiscuous helper T-cell peptide epitope; immunomimic peptide epitop breast cancer; uterine cancer; gynaecological cancer; endometriosis; uterine ancer; synaecological cancer; endometriosis; uterine fibroid; benign prostatic hypertrophy; prostate cancer.
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1. .10
'note= "Gonadotrophin releasing hormone epitope (1. aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID NO 7528; 71pp + Sequence Listing; English.
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                             Duclert A, Giordano J.;
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                                                                                                     21-FEB-2000; 2000EP-00200610.
                                                                                                                                            99US-0122487P.
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Best Local Similarity luv.
                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
N-PSDB; AAC03453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51 AA;
                                                                                                                                                                                       (GEST ) GENSET
                    EP1033401-A2.
                                                                                                                                              26-FEB-1999;
                                                             06-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia.
Synthetic.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH also known as luteinishing hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
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                                                                                                                                                                    42. 50
/note= "Gonadotrophin releasing hormone epitope (2-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                      "Other= Pyro-glutamic acid or 5-oxo proline"
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Similarity 100.0%; Score 29; DB 5; Length 50;
6; Conservative 0; Mismatches n. --3-1
                                                                                                                                                                                                                                                          /note= "Amidated glycine or glycinamide"
                                                                                   Human secreted protein, SEQ ID NO: 7528.
                                          11. .16
/note= "Spacer peptide"
                                                                                                                       .41
.41
r.e= "Spacer peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG03447 standard; protein; 51 AA.
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    /label= OTHER
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                           'note=
                                                                                                                                                     'note=
                                                                                                                                                                                                                  aa)"
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                     WO200185763-A2
                                                                                                                                                                                                                                        Modified-site
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RESULT 10 AAG03447

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The present invention relates to human single exon nuclear acts frows. (GENP: see AAI106B-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 22990; 487pp; English.
                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR
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                                                                                                                                                         26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                                                 30-JAN-2001; 2001WO-US000670
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                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
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                    WO200157278-A2.
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                            09-AUG-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a synthetic immunogen for inducing specific antibodies against gonadorropin releasing hormone (GnRH also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
                                                                                                                                                       43. 51
/note= "Gonadotrophin releasing hormone epitope (2-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #4598 encoded by probe for measuring cervical gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; microarray; gene expression; cervical epithelial cell;
                    "Other= Pyro-glutamic acid or 5-oxo proline"
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100.0%; Score 29; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                           11. .16
17. .36
/note= "Malaria CSP protein (378-398 aa)"
                                                                                                                                                                                                                                  /note= "Amidated glycine or glycinamide"
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16
ne= "Spacer peptide"
                                                                                                              37. .42
/note= "Spacer peptide"
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/label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-2000; 2000US-0202328P
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                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grimes S, Michaeli D,
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                                                                                                                                                                                                                Modified-site
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                                       Peptide
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Length 53; 0; Indels

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                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                  Claim 27; SEQ ID NO 29830; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                Length 53;
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100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
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                                                 Chen W, Rank
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2000US-0207456P.
2000US-0608408.
2000US-0533468.
2000US-0234687P.
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                             (MOLE-) MOLECULAR DYNAMICS INC
27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                         Local Similarity 100.
                                                 DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
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                                                                  WPI; 2001-483447/52
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                                                 Hanzel
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
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                                                 Penn SG,
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Matches
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring gene expression in
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , breast disease, breast cancer, development disorder, disease, proliferative breast disease, non-carcinoma
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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2000US-00632366.
2000US-0234687P.
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2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                             SSGPSL 10
                                                                                                                                                                                                                                                                                                                                                                    φ
                                                                                                                                                                                                                                                                                                                                                                       1 SSGPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human breast.
                                                                                                                                                                                                       Sequence 53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             ın
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM05786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe;
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SQ Sequence 53 AA;

0; Gaps Query Match
100.0%; Score 29; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

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1 SSGPSL 6

δ qq

Search completed: March. 10, 2004, 09:12:08 Job time : 11.035 secs

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32
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Q9uvt8 magnaporthe
Q9uyg1 homo sapien
Q8vel0 mus musculu
Q8d8y9 mus musculu
Q7syg6 xenopus lae
Q9fjx4 arabidopsis
Q8fxv6 mycobacteri
Q81xv0 homo sapien
Q91913 aeromonas v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q83f79 coxiella bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8yjl9 brucella me
Q7u3u5 synechococc
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Q86606 simian viru
                                                                                                                                                                         March 10, 2004, 08:58:54; Search time 5.92996 Seconds (without alignments) 319.245 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UUG1
Q8VEL0
Q9D8Y9
Q7SYQ6
Q9FUX4
Q8VKE5
Q8IXV0
Q9L913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8YJL9
Q7U3U5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8MZ01
Q9UVT8
                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_nman:*
sp_nman:*
sp_nwertebrate:*
sp_nammal:*
sp_nc:*
sp_organelle:*
sp_bhage:*
sp_lant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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29
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Q97h14 clostridium	07yve4 trypanosom	clostrid					P72605 synechocyst				Q9syz6 arabidopsi						Q9cvw5 mus musculu	ncep	mus		ara	Q9fus7 arabidopsis		aenorha	ď	ar	Q9fus9 arabidopsi	QBvcg7 mus muscu	
Q97H14	Q7YVE4	Q8XKM3	Q7TOR3	Q82M06	Q8FY77	Q7ZUA3	P72605	QBA6CB	Q8BP38	Q8PM63	9ZXS6Ö	Q8NM57	Q98K31	Q9EQJ5	Q89BU2	Q9SY80	Q9CVW5	Q8SW89	Q99PH9	Q99PI3	Q9SY78	Q9FUS7	09SXZ1	001786	Q9FUS8	Q94II0	Q9FUS9	Q8VCG7	
16	w	16	13	16	16	13	16	16	7	16	10	16	16	11	16	10	11	S	11	17	5	0	10	'n	10	10	10	11	
405	430	437	486	492	507	520	532	593	615	1009	1074	1197	2078	3262	103	121	123	183	189	189	192	207	218	222	227	227	227	227	
100.0	٦.	100.0	_	_	100.0	٠.	100.0	100.0	Ξ.		100.0	Ξ.	100.0	100.0	93.1		93.1	93.1	93.1	93.1	93.1	93.1				٠	93.1		
53	53	29	53	29	29	29	29	29	29	29	29	29	29	59	27	27	27	27	27	27	27	27	27	27	27	27	27	27	
17							24												36	37		39		41	42	43	44	45	

ALIGNMENTS

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STRAIN-Nine Mile phase I / RSA 493;

STRAIN-Nine Mile phase I / RSA 493;

MEDLINE-22608657; PubMed-12704232;

Seshadri R., Paulsen I.T., Elsen J.A., Read T.D., Nelson K.E.,

Nelson W.C., Mard N.L., Tettelin H., Davidsen T.M., Beanan M.J.,

DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.

Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,

Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

"Complete genome sequence of the Q-fever pathogen, Coxiella
burnetii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                   Coxiella burnetii.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 16; Length 113;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002110; ANK.

Hypothetical protein; Complete proteome.

SEQUENCE 113 AA; 12752 MW; 5C82A677DEE7BD95 CRC64;
                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
EMBL, AE016960, AA089636.1; -.
TIGR, CBU0069; -.
113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No.
                                                Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                     01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               burnetii
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Gaps

SSGPSL 40

1 SSGPSL 6

79 SSGPSL 84

Q8MZ01

RESULT 2
OGMAZO
ORAZO
OR

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C1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
RICOT-02003 (TrEMBLrel. 25, Last annotation update)
RIKEN CDNA 1810018L05 gene.
1810018L05RIK.
Buka musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                            Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 29; DB 11; Length 213; larity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 29; DB 4; Length 213; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Placenta;
TISSUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCO18129; AAH18329.1; -. MGD; MGI:1917630; 1810018L05Rik. GO; GO:005198; Fstructural molecule activity; IEA. InterPro; IPR00535; MSP domain. InterPro; IPR005952; PapD-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodes S., Huckle E.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein.
213 AA; 24086 MW; 2E0944F48058B47F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24074 MW; FB72756A0528CB34 CRC64;
                                                                                                                                 213 AA.
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00635; MSP doma-
PROSITE; PS50202; MSP;
SEQUENCE 213 AA; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Local 6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 SSGPSL 160
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSGPSL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                           Q9UJG1
Q9UJG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8VEL0
Q8VEL0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
RESULT 4
Q9UJG1
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Person K., Schneider G., Jordan D.B., Viitanen P.V., Sandalova T.;

RT "Comparison of the crystal structures of the pentameric fungal and the rorsahedral plant lumazine synthases.";

RI Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

RI Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

BR EL, AF148449, AADS5372.1; -..

BR EL, AF14849, AADS5372.1; -..

BR CO: GO:0009349; C:riboflavin synthase activity; IEA.

GO: GO:0004746; P:riboflavin synthase activity; IEA.

GO: GO:0009231; P:victamin B2 biosynthesis; IEA.

BR TIGRFANS DMRL synthase.

BR Pfam; PF00885; DMRL synthase; 1.

Probom; PD003664; DMRL synthase; 1.

Probom; PD003664; DMRL synthase; 1.

R TIGRFANS; TIGR00114; ribH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase.
Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha, Ebhydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 29, DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.18+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 29; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY113451; AAM29456.1; -. FlyBase; FBgn0063034; BcDNA:RE33542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA; 19281 MW; 05C5CE1AB43DB8DA CRC64;
                                                                                   Created)
Last sequence update)
Last annotation update)
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        174 AA
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                                                                               01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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            PRELIMINARY;
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